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OM protein - protein search, using sw model

Run on: November 23, 2005, 04:50:08 ; Search time 2.73403 Seconds
(without alignments)
203.984 Million cell updates/sec

Title: US-09-455-978B-77
Perfect score: 933
Sequence: 1 MSNDNDTIVTADVRNGIDGH..... DELVARFLPMLKULTFDQQI 184

Scoring table: BLOSUM62
Gapot 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
1: /cgn2_6/ptcodat/2/pupaa/US10_NEW_PUB.pep:/*
2: /cgn2_6/ptcodat/2/pupaa/US06_NEW_PUB.pep:/*
3: /cgn2_6/ptcodat/2/pupaa/US07_NEW_PUB.pep:/*
4: /cgn2_6/ptcodat/2/pupaa/US08_NEW_PUB.pep:/*
5: /cgn2_6/ptcodat/2/pupaa/US09_NEW_PUB.pep:/*
6: /cgn2_6/ptcodat/2/pupaa/PCT_NEW_PUB.pep:/*
7: /cgn2_6/ptcodat/2/pupaa/US11_NEW_PUB.pep:/*
8: /cgn2_6/ptcodat/2/pupaa/US60_NEW_PUB.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
US-10-858-730-2
; Sequence 2, Application US/10858730
; Publication No. US200502555601
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Truehart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorkey, Peter S.
; APPLICANT: Yorkey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 1184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,850
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Amycolatopsis mediterranei
US-10-858-730-2

Query Match 9.0%; Score 84; DB 1; Length 421;
Best Local Similarity 27.1%; Pred. No. 0.39; Mismatches 64; Indels 26; Gaps 8;
Matches 42; Conservative 23; Mismatches 64; Indels 26; Gaps 8;

Qy

Oy

Db

RESULT 2
US-10-793-626-456
; Sequence 456, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMELLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU340US
; CURRENT APPLICATION NUMBER: US/10/793, 626
; CURRENT FILING DATE: 2004-03-04
; PRIORITY APPLICATION NUMBER: 60/164, 258
; PRIORITY FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 456
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-456

Query Match 8.1%; Score 75.5; DB 1; Length 522;
Best Local Similarity 23.2%; Pred. No. 3;
Matches 49; Conservative 30; Mismatches 87; Indels 45; Gaps 9;
Qy 4 DNDTLVTAD--VRN---GIGHALADRIGDEAEIAWRLSFTGIDD----- 44
Db 145 DNVSLIKLDGKVKNFRVTKLFGYFGLKREEEEAQAGDLIAVGMDINVGETVPHDR 204
Qy 45 DTMAALAAEOPLFATADALVTDYDVFVHLESY---ERTQDIFANSTKVEQKET---QAE 98
Db 205 DPLPLVLRIDETMLETPFKVNNSPFAGREGDVTARQIOERLQQLETDVSLKVPTDQD 264
Qy 99 YLGLGLRGEYDTEYAAQRAR---IGKHDVVLGLGPDVYLGATRYVTLGLAD 151
Db 265 SWVAGRGELHLSILINMRREGFELQSK-----POVIL---REIDGVLSPEF 312
Qy 152 VVAD-RGEAAAVADLVARFLPMLKLLTFD 181
Db 313 VQCEVPSENAGAVIESLGAARKGEMLDMMTTD 343

RESULT 3
US-10-793-626-2042
; Sequence 2042, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMELLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU340US
; CURRENT APPLICATION NUMBER: US/10/793, 626
; CURRENT FILING DATE: 2004-03-04
; PRIORITY APPLICATION NUMBER: 60/164, 258
; PRIORITY FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2042
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2042

Query Match 8.1%; Score 75.5; DB 1; Length 724;
Best Local Similarity 23.1%; Pred. No. 4.5; Matches 48; Conservative 28; Mismatches 75; Indels 57; Gaps 11;
Qy 4 DNDTLVTADYRNGIDGHALADRIGDE--AEIAWRLSFTQIDDTMALAAEOPLFETA 61
Db 111 DNDVQKEDQDINKI-VHILANEADTKIAEDQNYDVGELKBLNVI----- 158
Qy 62 DALVTDYDYLIESYERTQDLFANSTKTVQELKETOAEVYLGIGRGEY--DTEYAAQRAR-- 118
Db 159 -----YHIEERLTLKDI-SNKLYVSKSNLSTQPHLLGGMFKYIDTLKISKIEML 210
Qy 119 -----IGKHDVVLGIG-----POVILGATRY--YTGILDAADDVA 154
Db 211 LTTTKNSIQSETLRSVNTSYRSRQPKVYLSVTRAY-RAMKCDKNGSD--DDV-- 264
Qy 155 DRGEAAVADLVARFLPMLKLLTFD 182
Db 265 --SEHLKSCVQSLCISCKMPNEDNYE 290

RESULT 5
US-11-045-802-29
; Sequence 29, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
; APPLICANT: Gordon-Kamm, William
; APPLICANT: Helentjaris, Tim
; APPLICANT: Lowe, Keith
; APPLICANT: Shen, Bo
; APPLICANT: Tarcynski, Mitchell
; APPLICANT: Zheng, Peizhong
; TITLE OF INVENTION: Ap2 Domain Transcription Factor ODP2 (Ovule Development Protein 2 and Methods of Use
; TITLE OF INVENTION: and Methods of Use
Query Match 8.1%; Score 75.5; DB 1; Length 522;
Best Local Similarity 23.2%; Pred. No. 3;
Matches 49; Conservative 30; Mismatches 87; Indels 45; Gaps 9;
Qy 4 DNDTLVTAD--VRN---GIGHALADRIGDEAEIAWRLSFTGIDD----- 44

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; FILE REFERENCE: 035718/286074
; CURRENT APPLICATION NUMBER: US/11/045, 802
; CURRENT FILING DATE: 2005-01-28
; PRIORITY APPLICATION NUMBER: 60/541, 122
; PRIORITY FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-11-045-802-29

; QUERY Match 8.0%; Score 75; DB 7; Length 655;
; Best Local Similarity 22.4%; Pred. No. 4.4; Mismatches 50; Indels 48; Gaps 7;
; Matches 35; Conservative 23; Mismatches 50; Indels 48; Gaps 7;

; QY 41 GIDDDTMALAAEQLFEATADALVTDYDHLESYERTQDLFANSTKIVEQJK-EQAEY 99
; Db 314 GKDKEEKARAYDIAALKWGTNTF-PMSNEY-----KEVEENKHMTRQEY 361
; QY 100 LLG-----GRGEY-----DTEYEAQRARIGKHDVGLGPDVYLGAATRYVGLL 145
; Db 362 IAHLRNNSGFSRGASKYRGVTRHHOGRWQARIGRVA---NKDLYLGT----- 410
; QY 146 DALADDVADRGEEAAAVDELVARFPLMULTFD 181
; Db 411 -----TEBAAEAYDIAIKFRGGINAVTNFD 436
; Db -----US-11-045-802-31

; RESULT 6
; US-11-045-802-30
; Sequence 30, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
; APPLICANT: Gordon-Kamm, William
; APPLICANT: Helen-Jaris, Tim
; APPLICANT: Lowe, Keith
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell
; APPLICANT: Zheng, Peizhong
; TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2)
; FILE REFERENCE: 035718/286074
; CURRENT APPLICATION NUMBER: US/11/045, 802
; PRIORITY APPLICATION NUMBER: 60/541, 122
; PRIORITY FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-11-045-802-31

; QUERY Match 7.9%; Score 74; DB 7; Length 584;
; Best Local Similarity 23.7%; Pred. No. 4.7; Mismatches 53; Indels 48; Gaps 7;
; Matches 37; Conservative 18; Mismatches 53; Indels 48; Gaps 7;

; QY 41 GIDDDTMALAAEQLFEATADALVTDYDHLESYERTQDLFANSTKIVEQJK-EQAEY 99
; Db 248 GKDKEEKARAYDIAALKWGTNTF-PLSEYE-----KEVEENKHMTRQEY 295
; QY 100 LL-----GLGRG-----DTEYEAQRARIGKHDVGLGPDVYLGAATRYVGLL 145
; Db 296 VASLRKNSGFSRGASKYRGVTRHHOGRWQARIGRVA---NKDLYLGT----- 343
; QY 146 DALADDVADRGEEAAAVDELVARFPLMULTFD 181
; Db 344 -----GTOBEAAEAYDIAIKFRGGLSAVTNFD 370
; Db -----US-11-045-802-32

; RESULT 8
; US-11-045-802-32
; Sequence 32, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
; APPLICANT: Gordon-Kamm, William
; APPLICANT: Helen-Jaris, Tim
; APPLICANT: Lowe, Keith
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell
; APPLICANT: Zheng, Peizhong
; TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2)
; FILE REFERENCE: 035718/286074
; CURRENT APPLICATION NUMBER: US/11/045, 802
; PRIORITY APPLICATION NUMBER: 60/541, 122
; PRIORITY FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Brassica napus
; US-11-045-802-32

; QUERY Match 7.8%; Score 73; DB 7; Length 579;
; Best Local Similarity 23.1%; Pred. No. 5.8; Mismatches 53; Indels 48; Gaps 7;
; Matches 36; Conservative 19; Mismatches 53; Indels 48; Gaps 7;
; SEQ ID NO 34
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Brassica napus
; US-11-045-802-33

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QY 41 GIDDDTMALAAEQPFEATADALVTDYDHESYERTQDLFANSTKTYVEQKE-TQAEY 99
Db 248 GYDKEKARAYDAAALKYWGTTTTNF--PNSYE-----KEVEEMKHMTRQEY 295
QY 100 LL-----GLRG-----EVDEYAAQRARIGKHDVGLGPDVYLGATRYTGYLL 145
Db 296 VASLRKSGFSGFSGASITYRGVTRHHQHGRWQARIGRIVAG---NKDLYLGT----- 343
QY 146 DALADDVWADRGEEAAAVDELVARFLPMLKLTFD 181
Db 344 -----GTQBEAAEYDIAIKFRGLTAVINFD 370
; SEQ ID NO 33
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Brassica napus
; US-11-045 802-33
Query Match 7.7%; Score 72; DB 7; Length 579;
Best Local Similarity 22.4%; Pred. No. 7,1; Mismatches 53; Indels 48; Gaps 7;
Matches 35; Conservative 20;
FILE REFERENCE: 14184-030001
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIORITY APPLICATION NUMBER: US 60/475,000
; PRIORITY FILING DATE: 2003-05-30
; PRIORITY APPLICATION NUMBER: US 60/551,860
; PRIORITY FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-10-858-730-292
RESULT 9
US-10-858-730-292
; Sequence 292, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Vorsey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIORITY APPLICATION NUMBER: US 60/475,000
; PRIORITY FILING DATE: 2003-05-30
; PRIORITY APPLICATION NUMBER: US 60/551,860
; PRIORITY FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-10-858-730-292
RESULT 10
US-11-045 802-33
; Sequence 33, Application US/11045802
; Publication No. US20050257289A1
; GENERAL INFORMATION:
; APPLICANT: Gordon Kamm, William
; APPLICANT: Helent Karis, Tim
; APPLICANT: Lower, Keith
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell
; APPLICANT: Zheng, Peizhong
; TITLE OF INVENTION: Ap2 Domain Transcription Factor ODP2 (Ovule Development Protein 2
; FILE REFERENCE: 135718/286074
; CURRENT APPLICATION NUMBER: US/11/045,802
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-10-858-730-72
Query Match 7.6%; Score 71; DB 1; Length 1192;
Best Local Similarity 26.5%; Pred. No. 21; Mismatches 34; Indels 36; Gaps 6;
Matches 31; Conservative 16; Mismatches 34; Indels 36; Gaps 6;
QY 57 FEATADALVTDY-----DHLEY-----ERTODLFANSTKTYVEQKE-----TQAEYLLG-L 103
Db 68 FEAGADAEVNTGCGNLNSQGDIADIRDLSQKGTRARRIADELGSPDRKRYVLSM 127
QY 104 GRGEY-----DTEYAAQRARIGKHDVGLGPDVYLGATRYTGYLLPDLADDDVAD 155
Db 128 GPSTKLPLTGHTEYAVIR-----DAYTEAALGMLDQGDAALIVE 166

RESULT 12

US-10-858-730-67

; Sequence 67, Application US/10858730

; Publication No. US20050255568A1

; GENERAL INFORMATION:

; APPLICANT: Bailey, Richard B.

; APPLICANT: Blomquist, Paul

; APPLICANT: Doten, Reed

; APPLICANT: Driggers, Edward M.

; APPLICANT: Madden, Kevin T.

; APPLICANT: O'Leary, Jessica

; APPLICANT: O'Toole, George

; APPLICANT: Trueheart, Joshua

; APPLICANT: Walbridge, Michael J.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID

; TITLE OF INVENTION: PRODUCTION

; FILE REFERENCE: 14184-030001

; CURRENT APPLICATION NUMBER: US/10/858, 730

; CURRENT FILING DATE: 2004-06-01

; PRIORITY FILING DATE: 2003-05-30

; PRIORITY APPLICATION NUMBER: US 60/551, 860

; PRIORITY FILING DATE: 2004-03-10

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 67

; LENGTH: 530

; TYPE: PRT

; ORGANISM: Streptomyces coelicolor

; US-10-858-730-67

; QUERY Match

; Best Local Similarity

; Score 70.5; DB 1; Length 530;

; Matches

; 47; Conservative

; 24; Mismatches

; 72; Indels

; 73; Gaps

; 10;

; QY

; 6

; DTLYTADYNGIDGICHALADRIGLDEA-----IAHR-----LS

; 38

; Db

; 285

; DTTVPDSANQPYDPMHSVIRV-LDDAEFTQPLFAPNPLTGFGVRGEGRPVGIVANQPMQ

; 343

; QY

; 39

; FTGIDDDTMALAAEAQPLFEATADL--WTDYFD--HLESTERTQD-----LFA

; 83

; Db

; 344

; FAGCDITASKEAAR--FVRTCDAFNPNVPLTFVDPVGPFLPGVDOEHGIRIRRAGKLIA

; 400

; QY

; 84

; NSTKVEQLEKTOAQEYLGLGGRGEVTEVAQARARIGKIHDLVIG--LGPPDVILGAYTRY

; 140

; Db

; 401

; YAETVPLT-----VITRAFGGGIYDVGMSKHLGADLNUAWPRAQ

; 441

; QY

; 141

; YT----GLDADLADDWDRGEREAAAVDELVLF

; 171

; Db

; 442

; IAWMGAQGAVANILHRRTIADAGDDEAETRARIQY

; 477

RESULT 14
 ; SEQ ID NO: 28
 ; LENGTH: 597
 ; TYPE: PRT
 ; ORGANISM: oryza sativa
 ; US-11-045-802-28
 ; QUERY Match
 ; Best Local Similarity

7.6%; Score 70.5; DB 7; Length 597;

; Matches

33; Conservative

17; Mismatches

42; Indels

51; Gaps

6; QY

69 YDHLSESTERTQDFA-----NSKTVUELIKE-TQAEVIL-----GIGR

105

Db

319 YDKEKAARAYDAALKWGPFTTTFPVNNYKELEMKHMTRQEVASLRKSSGFSR

378

QY

106 G-----BYDTEVAQARARIGKIHDLVGLGPFLPGVTRYTGILDAADDVALDRB

158

Db

379 GASTYRVTRHIGRWRGARIGRVAG---NKOLYLSRSTQ-----E

417

QY

159 EAAMAVDELVARFLPMLKLTED

181

Db

418 EAAYDIAAIKFRGLNAVTFD

440

RESULT 14
 ; SEQ ID NO: 26
 ; LENGTH: 692
 ; TYPE: PRT

US-11-045-802-26
 ; Sequence 26, Application US/1045802
 ; Publication No. US20050257289A1

; GENERAL INFORMATION:

; APPLICANT: Gordon-Kamm, William

; APPLICANT: Helensjari, Tim

; APPLICANT: Lowe, Keith

; APPLICANT: Shen, Bo

; APPLICANT: Tarczynski, Mitchell

; TITLE OF INVENTION: AP2 Domains Transcription Factor ODP2 (Ovule Development Protein)

; TITLE OF INVENTION: and Methods of Use

; FILE REFERENCE: 033718/286074

; CURRENT APPLICATION NUMBER: US/11/045, 802

; CURRENT FILING DATE: 2005-01-28

; PRIORITY FILING DATE: 2004-02-02

; PRIORITY FILING DATE: 2004-02-02

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 26

; LENGTH: 692

; TYPE: PRT

; ORGANISM: Oryza sativa

; US-11-045-802-26

; QUERY Match

; Best Local Similarity

; Score 70.5; DB 7; Length 692;

; Matches

; 33; Conservative

; 17; Mismatches

; 42; Indels

; 51; Gaps

; 6; QY

; 69 YDHLSESTERTQDFA-----NSKTVUELIKE-TQAEVIL-----GIGR

; 105

; Db

; 319 YDKEKAARAYDAALKWGPFTTTFPVNNYKELEMKHMTRQEVASLRKSSGFSR

; 378

; QY

; 106 G-----BYDTEVAQARARIGKIHDLVGLGPFLPGVTRYTGILDAADDVALDRB

; 158

; Db

; 379 GASTYRVTRHIGRWRGARIGRVAG---NKOLYLSRSTQ-----E

; 417

; QY

; 159 EAAMAVDELVARFLPMLKLTED

; 181

; Db

; 418 EAAYDIAAIKFRGLNAVTFD

; 440

; RESULT 15

; US-11-045-389-90

; Sequence 90, Application US/11082389

; Publication No. US20050244935A1

; GENERAL INFORMATION:

; APPLICANT: Pompejus, Markus

; APPLICANT: Kroger, Burkhard

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; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487,4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489,0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549,3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550,7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134,5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379,7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 90
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-11-082-389-90

Query Match 7.4%; Score 69.5; DB 7; Length 360;
Best Local Similarity 23.7%; Pred. No. 6,8; Matches 45; Conservative 33; Mismatches 81; Gaps 10; Indels 31; Gaps 10;
Matches 45; Conservative 33; Mismatches 81; Gaps 10; Indels 31; Gaps 10;
QY 2 SNDNDTUVTAQYRNGIDGHAIADRIGDEAETAWRLSFTGIDDDTMALAABEQLFEATA 61
Db 35 SNNSAKTTA----LNVLT---VEPGEVIGIGYSGACKSTLVRLI--NGLDSPTS 83
QY 62 DALV--TDFVQHLESVERTQDFLANSKTKTVEQKETQAEVLLGLGRGEYETY----A 113
Db 84 GSLLNGTDRIVGMPES--KLRIKURSNIGMIVQFNLFOSR--TAAGNVEYLLEVAKNDKA 139
QY 114 AQRARICKIHIVDVLGLG----PDVYLGAYTRYYTGILDALADDVVAADRGEAAAD-E 166
Db 140 ARKARVQEMLERVGLGDKGKQNVPEQLSGG-QKQRVGiarALATNPILLADBATSALDE 198
QY 167 LYARFLPMK 176
Db 199 TTHEVBLLR 208

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Search completed: November 23, 2005, 05:09:26
 Job time : 3.28403 secs

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Om protein - protein search, using sw model
Run on: November 23, 2005, 04:37:11 ; Search time 18.0446 Seconds
(without alignments) 843.041 Million cell updates/sec

Title: US-09-455-978B-77
Perfect score: 933
Sequence: 1 MSNDNDLTAVDRNGIDH..... DELVARFLPMLKULTFDQOI 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.5	10.1	396	2	US-09-902-540-10455
2	91.5	9.8	955	1	US-08-420-414A-3
3	89	9.5	955	1	US-08-420-476B-1
4	89	9.5	955	1	US-08-282-845-2
5	89	9.5	955	4	PCT-US94-00324-1
6	86.5	9.3	318	2	US-09-710-262B-14
7	83.5	9.2	302	2	US-08-328-352-4846
8	83.5	8.9	319	2	US-09-489-039A-8872
9	83.5	8.9	640	2	US-09-241-602B-31
10	82.5	8.8	831	2	US-09-605-703B-1396
11	82	8.8	329	2	US-10-622-064-28
12	82	8.8	542	2	US-09-252-991A-21396
13	81.5	8.7	1253	2	US-09-252-991A-3019
14	80.5	8.6	700	2	US-09-252-991A-19384
15	80	8.6	553	2	US-09-252-991A-32970
16	80	8.6	677	2	US-09-252-991A-1902
17	79	8.5	438	2	US-09-540-236-2595
18	79	8.5	592	2	US-09-902-540-15457
19	79	8.5	878	2	US-08-941-936-2
20	78.5	8.4	733	2	US-09-328-352-5599
21	78.5	8.4	755	4	PCT-US93-07923-3
22	78.5	8.4	759	4	PCT-US93-07923-2
23	78.5	8.4	766	1	US-08-230-491A-3
24	78.5	8.4	766	1	US-08-619-2280A-3
25	78.5	8.4	766	1	US-08-90-391-3
26	78.5	8.4	766	2	US-09-794-236-1
27	78.5	8.4	766	2	US-10-002-593-6

ALIGMENTS

RESULT 1
US-09-902-540-10455
; Sequence 10455 Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 3B-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-7-10
; PRIORITY APPLICATION NUMBER: 60/217,883
; PRIORITY FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO: 10455
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-10455

Query Match 10.1%; Score 94.5; DB 2; Length 396;
Best Local Similarity 23.3%; Pred. No. 0.028; Mismatches 81; Index 23; Gaps 5;
Matches 40; Conservative 28; Mismatches 81; Index 23; Gaps 5;

QY 32 EIAWRLLSTGIDDMMAL-AAEQPLEATADALVTPYDHLSEYETQDILFANSTKIVTE 90
Db 8 ELKRYVGFSSADQALVNTATHAKPFRFARV---FYDRILEHEGARQALEGGESQVG 63

QY 91 QLKETQAFLIGLGRGEDEMTMAQARAFRIGKHDVLSGQPDVILGAT-- RYVGLDJA 147
Db 64 HLRGTLQWMDQQLRGPRDVEVYALRGRIGMVRALPQHNGAMNLROBNFNSHIDA 123

QY 148 -LADDVADRGEEAAAV----- DELVARFLPMLKULTFDQOI 184
Db 124 TYLBEPAPARAAKSARAVKILDELMINTYREDLQARSRSLSTFGQLY 175

RESULT 2
US-08-428-414A-3
; Sequence 3, Application US/08428414A
; Patent No. 5912166
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TITLE OF INVENTION: LISHMANIASIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY

STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/128,414A
 FILING DATE: 21-APR-1995
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Radicek, Ann T.
 REGISTRATION NUMBER: 39,244
 REFERENCE/DOCKET NUMBER: 210121,407
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEX: 3723936 SEDBANDBERRY
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 955 amino acids
 TYPE: amino acid
 STRANDEDNESS: Linear
 TOPOLOGY: Linear
 US-08-428-414A-3

Query Match 9.8%; Score 91.5; DB 1; Length 955;
 Best Local Similarity 27.3%; Pred. No. 0.24; Mismatches 77; Indels 45; Gaps 8;
 Matches 54; Conservative 22; Mismatches 77; Indels 45; Gaps 8;

Qy 13 VRNGTGHALADRIGDEAETAWRLSFTGIDDDTMALAAATQPLFRTADALV---DFY 69
 Db 530 VRRRLDREIAABREKL|-----ESTVAQLERQRREREVALIDQTHORKLQ 574
 Qy 70 DHLESVERTOOLFANSKTKVQLEKETOAEVYLGIGGEYDE-YAQRARIGKIHDLVGL 128
 Db 575 EALESSBERTA---AERDQLQOLTELQOSE-RTQLSQVVTDRBLTRDQLQIYQEVGETEL 630

Qy 129 GPDVYIIGA---YTRYTYGLI-----DALADDVADRGEEAAAVDELV--- 168
 Db 631 ARDVALCAAQMEYHAAVPHLQLTLEATEWEDALRERLAERDEAAEELDAASTS 690
 Qy 169 ---ARFLPMLKLTDFQOI 184
 Db 691 QNARESACERLTSLEQOL 708

RESULT 3
 US-08-006-676B-1
 Sequence 1: Application US/08006676B
 Patent No. 5511965
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 TITLE OF INVENTION: A 23Kd Antigen Present in Leishmania
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ImmuneX Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

RESULT 3
 US-08-006-676B-1
 Sequence 1: Application US/08006676B
 Patent No. 5511965
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 TITLE OF INVENTION: Diagnosis of Leishmaniasis
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jeffrey B. Oster
 STREET: 8339 SE 57th Street
 CITY: Mercer Island
 STATE: Washington
 COUNTRY: USA
 ZIP: 98040-4906
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word for Macintosh Operating System 7.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/282,845
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 5004-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEX: (206) 233-0644
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 955 amino acids


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Db 235 KSSSIKWWIVSYDNVDAIREIYKDFRV---LEYSLOQYTAQOKKIGEEVMFTSNDV-LI 288
Qy 130 PDVYLG 135
Db 289 PNVRLG 294
; ORGANISM: Piscirickettsia salmonis
; US-10-241-602B-31
RESULT 8
; Sequence 8872, Application US/09489039A
; Patent No. 6510836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709 2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; SEQ ID NO 8872
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-8872

Query Match 8.9%; Score 83.5; DB 2; Length 319;
Best Local Similarity 25.4%; Pred. No. 0.39; Mismatches 72; Indels 61; Gaps 9;
Matches 51; Conservative 17; Mismatches 72; Indels 61; Gaps 9;
Qy 14 RNGIDGHALADRIGLDEAIA-WRLSFTGIDDDTMALAAEQPLF-----EATDALV 65
Db 120 RRNIDGVVLFGFTGIDBAMLAAPWR-----DTLVLMARDAPGFASVCDTDEGATLIM 171
Qy 66 TDFYDH-----LESVERTQDILFANSTKIVQEQLKEAQBYLIGLGRGYDTE 111
Db 172 ORLYDRGRHRHSFLGVPHSDVVTGERRHLAVLAFCKKR-HRUTPTAALPGLGKQG-YDTV 229
Qy 112 YAAQRARIGK-----HDVVLGIGSDPVLYGATRYTGLDAL----- 148
Db 230 ASVLATTSAVCATDLAGTASLYQQR-----DALQASVGSTPLMKFLHEILT 283
Qy 149 ADDVVADRGEEAAVDELVA 169
Db 284 VDPGYAESGRARQLEQIA 304

RESULT 9
; Sequence 31, Application US/10241602B
; Patent No. 6887989
; GENERAL INFORMATION:
; APPLICANT: Simard, Nathalie
; APPLICANT: Brouwers, Huub
; APPLICANT: Jones, Simon
; APPLICANT: Griffiths, Steve
; APPLICANT: Valenzuela, Pablo
; APPLICANT: Burzio, Luis
; TITLE OF INVENTION: Sequences from Piscirickettsia salmonis
; FILE REFERENCE: H-32319A
; CURRENT APPLICATION NUMBER: US/10/241, 602B
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: PCT/GB01/01055
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: GB0005838.8
; PRIOR FILING DATE: 2000-03-11
; PRIOR APPLICATION NUMBER: GB0016080.4
; PRIOR FILING DATE: 2000-07-01
; PRIOR APPLICATION NUMBER: GB0016082.0
; PRIOR FILING DATE: 2000-07-01
; PRIOR APPLICATION NUMBER: GB0016599.1
; PRIOR FILING DATE: 2000-07-29

; US-10-241-602B-31
; Sequence 1396, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: Corynebacterium glutamicum GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605, 703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142, 764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152, 318
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1396
; LENGTH: 831
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-605-703B-1396
Query Match 8.8%; Score 82.5; DB 2; Length 831;
Best Local Similarity 25.4%; Pred. No. 2.1; Mismatches 46; Conservative 25; Mismatches 81; Indels 29; Gaps 8;
Matches 46; Conservative 25; Mismatches 81; Indels 29; Gaps 8;
Qy 7 TLTVA--VFNG---QLDQHQDYEV--RAMYALNDRSNLARDGL-----DNKOS 532
Db 486 TLTVA--VFNG---QLDQHQDYEV--RAMYALNDRSNLARDGL-----DNKOS 532
Qy 67 DRYDHLESVYRTQDILFANSTKIVQEQLKEAQBYLIGLGRGYE-DTEYAMQRIGKHDV 125
Db 533 EFYEVYRRAEISDRDQMGDQQRVEERQQLQOEYANBEMAYKIAEQRVEYDRRH- 590
; 533 EFYEVYRRAEISDRDQMGDQQRVEERQQLQOEYANBEMAYKIAEQRVEYDRRH- 590
Qy 126 LGLGP--DVVLYGATRYTGLDALADVV-----ADRGEAAVADELVARFLPML 175
Db 591 --MPRTASLEAVGRETSURDRTIEDYFARMNTLRARAGERANAAESRIIDLRPIV 647
Qy 176 K 176
;
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Db 648 E 648

RESULT 11

US-10-622-064-28

; Sequence 28, Application US/10622064

; Patent No. 6932971

; GENERAL INFORMATION:

; APPLICANT: Bachmann, Martin F

; TITLE OF INVENTION: Haptен-Carrier Conjugates and Uses Thereof

FILE REFERENCE: 1700.0300001

CURRENT APPLICATION NUMBER: US/10/622,064

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: US 60/396,575

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.2

SEQ ID NO: 28

LENGTH: 329

TYPE: PRT

US-10-622-064-28

Query Match 8.8%; Score 82; DB 2; Length 329;

Best Local Similarity 24.5%; Pred. No. 0.61; Mismatches 61; Indels 42; Gaps 6; Matches 39; Conservative 17; Mismatches 61; Indels 42; Gaps 6;

Qy 37 LSTGIDDPMALAAEOPLEFEATADALVTDYDHLSEYERTQDLFANS-----T 86

Db 93 LSTGIDDPMALAAEOPLEFEATADALVTDYDHLSEYERTQDLFANS-----T 86

Qy 87 KTVQELKETQAEVYLGLGRGEYETEYAAQRARIGKHDVGLG-PDVVLGAVTRYVYGL 145

Db 152 PAVPVDPVKPD-----GTGRYKCPFACT--RGSISIVGKGSQPDY----- 190

Qy 146 DALADDVVADRGEEAAAADVDELVARFLPMLKULLTDDOII 184

Db 191 -----ERGDEVSVTFDVALEDFLGLNTNWNRNWDQRL 220

RESULT 12

US-09-252-991A-21396

; Sequence 21396, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO: 30019

LENGTH: 1253

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30019

Query Match 8.7%; Score 81.5; DB 2; Length 1253;

Best Local Similarity 22.5%; Pred. No. 5.1; Mismatches 75; Indels 59; Gaps 11; Matches 48; Conservative 31; Mismatches 75; Indels 59; Gaps 11;

Qy 2 SNDNDTLYTAD-VRNGDGHALADRIGCDEABIAWRSLFTGDDTMALAAEOPLEFEAT 60

Db 1024 SGHDHROHAELFELHALDGE--DRRLQVEVE-----DGLDQDQVGA----AFDQA 1068

Qy 61 ADALVTDYDHLSEYERTQDLF-----ANSTKTVQELKETQAEVYLGLG 104

Db 1069 ASRDLVWHLHOFVEGDDVAVAGVYHVRGHRAGAAGRAEHAGDEARLVRGIGGLRVRHLQQA 1128

Qy 105 RGYDTEYAAQRARIGKHDVGLG-----PDVVLGAVTRYVYGLDALLADYVA 154

Db 1129 R-PFREVFGQR-----LHAVOLGHGGVCGVGLGVAGY---EVGLDGL-DRVRA 1177

Qy 155 DRGEAAA-----VDBLVARFLPMLKULLTDDOII 181

Db 1178 AQQEVVVAFHVARPVGEALAAVVGFLQQLVALD 1210

RESULT 14

US-09-252-991A-19384

; Sequence 19384, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO: 19384

LENGTH: 542

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21396

Query Match 8.8%; Score 82; DB 2; Length 542;

Best Local Similarity 25.3%; Pred. No. 1.3; Mismatches 66; Indels 60; Gaps 8; Matches 49; Conservative 19; Mismatches 66; Indels 60; Gaps 8;

Qy 3 NNDPLVLTAVRNGDGHALADRIGLGLDEABIAWRSLFTGDDTMALAAEOPLEFEAT 62

Db 149 NNDPLVLTAVRNGDGHALADRIGLGLDEABIAWRSLFTGDDTMALAAEOPLEFEAT 62

Qy 63 ALVTD--FVHLSSEYERTQDLFANSTKVEQELKETQAEVYLGLGRGEYETEYAAQR-A 117

; ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-19384

Query Match 8.6%; Score 80.5; DB 2; Length 700;
Best Local Similarity 24.6%; Pred. No. 2.8;
Matches 49; Conservative 21; Mismatches 82; Indels 47; Gaps 8;
Matches 49; Conservative 21; Mismatches 82; Indels 47; Gaps 8;
Qy 12 DYRNGTDGHALADRIGLDEATEAWRLSFTGIDDDTMALAJAQPLFEATADALV---TDF 68
Db 129 DARRPDAHAPVPGQRAF-QATLAQR -----QVTATAAQRQLALAAGDVAQHRTQY 180
Qy 69 YDHLFESTRTDOLFLANSTKTFQKLKTOAEYLLIGRGEYETEYAAQRARGK1-HDVLG 127
Db 181 AERHQDQDEQHABHLDDVPEPRLRVERNAVDLFLGLGRGERRVHDHADAVAAAGVVAIRVL- 239
Qy 128 LGPDVVLGAYTRYTGTGIDALAD-----DV-----VADRGEE- 159
Db 240 -----YQAGEARQFVAGPLVADLAGLRLV-----WPHHRHRSQAQASILLGVAQWF 294
Qy 160 -AAAAYDELVALRFLPMKLL 177
Db 295 WVAGGLVALVGRVRRQQLRL 313

RESULT 15

US-09-252-991A-32970

; Sequence 32970, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILING REFERENCE: 107156.136

; CURRENT APPLICATION NUMBER: US/09-252, 991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074, 788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094, 190

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 32970

; LENGTH: 553

; TYPE: PRT

; ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-32970

Query Match 8.6%; Score 80; DB 2; Length 553;
Best Local Similarity 21.1%; Pred. No. 2.2;
Matches 41; Conservative 28; Mismatches 79; Indels 46; Gaps 5;

Qy 20 HALADRT----GLDEAEIARLUSFTGIDDDTMALAJAQPLFEATADALVTDFYHLES 74
Db 137 HAPAPRLLVSAFFLDAVAVLGLGPAVEGLAVLDEVVAQAGQRLPSSFAESAEBQRVIRRAA 196
Qy 75 VERTQDFPANSIKTKEQKLKTE---YLGIGLGRGRBYDTSYAQ-----RARIK- 121
Db 197 LHALQQLDQGLVLRSDAQAQPAHQVEVGVGEGQVHAGAQFVHFRQWORLQGOG 256
Qy 122 -----IHDVL-----GLGPDVVLGAYTRYTGTGIDALADDV 153
Db 257 QVPMGDYLVAGVAGVGVVADVIGVEVIRSEGVPVNEGNAEDRHVGVHHPVRAAIG 316
Qy 154 ADRGEERAAYAVNRL 167
Db 317 LPAGDEFGVALLDL 330

Search completed: November 23, 2005, 04:51:24
Job time : 23.0446 secs

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Om protein - protein search, using sw model

Run on: November 23, 2005, 04:50:03 ; Search time 60.1486 Seconds
(without alignment) ; 1278.178 Million cell updates/sec

Title: US-09-455-978B-77
Perfect score: 933
Sequence: 1 MSNDNTLVTDVRNGIDCH..... DELVARFLPMLKLTFDQIQI 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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2: /cgn2_6/ptodata/1/pubpaal/us08_PUBCOMB.pep: *
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4: /cgn2_6/ptodata/1/pubpaal/us10_PUBCOMB.pep: *
5: /cgn2_6/ptodata/1/pubpaal/us10b_PUBCOMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	99	10.6	448	4	US-10-460-524-5	Sequence 5, Appli
2	97.5	10.5	138	4	US-10-460-524-5	Sequence 3487, A
3	94.5	10.1	404	4	US-10-460-524-5	Sequence 18563, A
4	94	10.1	218	4	US-10-460-524-5	Sequence 9201, AP
5	89.5	9.6	400	4	US-10-460-524-5	Sequence 12480, A
6	89	9.6	400	5	US-10-460-524-5	Sequence 10618, A
7	88	9.4	505	4	US-10-460-524-5	Sequence 66025, A
8	87	9.3	496	4	US-10-460-524-5	Sequence 63364, A
9	86.5	9.3	318	5	US-10-460-524-5	Sequence 14841, AP
10	86	9.2	362	4	US-10-460-524-5	Sequence 137315, A
11	85	9.1	2703	4	US-10-460-524-5	Sequence 66018, A
12	84	9.0	163	4	US-10-460-524-5	Sequence 98, APPL
13	84	9.0	258	4	US-10-460-524-5	Sequence 287808, A
14	83.5	8.9	258	4	US-10-460-524-5	Sequence 11335, A
15	83.5	8.9	315	4	US-10-460-524-5	Sequence 59961, A
16	83.5	8.9	367	4	US-10-460-524-5	Sequence 7293, A
17	83.5	8.9	368	4	US-10-460-524-5	Sequence 48921, A
18	83.5	8.9	640	5	US-10-460-524-5	Sequence 31, APPL
19	83.5	8.9	1254	4	US-10-460-524-5	Sequence 53778, A
20	83.5	8.9	4384	5	US-10-460-524-5	Sequence 3638, AP
21	83	8.9	319	6	US-10-460-524-5	Sequence 13032, A
22	83	8.9	384	4	US-10-460-524-5	Sequence 48636, A
23	82.5	8.8	403	4	US-10-460-524-5	Sequence 61978, A
24	82.5	8.8	695	4	US-10-460-524-5	Sequence 69332, A
25	82.5	8.8	765	4	US-10-460-524-5	Sequence 13229, A
26	82.5	8.8	831	3	US-10-460-524-5	Sequence 5468, AP
27	8.8		928	4	US-10-460-524-5	Sequence 61748, A

ALIGNMENTS

RESULT 1

US-10-460-524-5

; Sequence 5, Application US/10460524
; Publication No. US2004029781A1
; GENERAL INFORMATION:
; APPLICANT: Jenkins, Elizabeth
; APPLICANT: Hernan, Ronald A
; APPLICANT: Mehigan, Richard J
; APPLICANT: Brooke, Ian
; APPLICANT: Jenkins, Elizabeth
; TITLE OF INVENTION: Affinity Peptides and Method for Purification of Recombinant Protein
; FILE REFERENCE: SEQ 70471
; CURRENT APPLICATION NUMBER: US/10-460-524
; CURRENT FILING DATE: 2003-06-12
; PRIORITY FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Streptococcus

US-10-460-524-5

Query Match Best Local Similarity 10.6%; Score 99; DB 4; Length 448; Matches 48; Conservative 25; Mismatches 45; Indels 72; Gaps 8;

QY 10 TADVRNGIDGHALADRIGDILBEARIWNLUSFTGIDD-----DTMALLAEE----- 53
Db 41 TPTIRNGER--LTNLGNSETTALRNNEESATDLRAAVADTVRAAENAGAAWEA 97

QY 54 ---QPLFATADAL-----VTDVFDLHESYERTQDLPANSTKTEQVQK 102
Db 98 AAAADALAKAKADAIKEFNKYGVSYDKYLN-----INNAKTVGIKOLQAQV-- 145

QY 103 LGRGEYDPEYAAQRARIGKIHVDLGLGPDVWLGAYTRVYTGILDAADDVADRGEEAA 162
Db 146 -----ESAKKARSEATD-----GLSDFLKSQTPA--EDTVK 175

RESULT 2

US-10-460-524-5

; Sequence 34787, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(5535)B
 CURRENT APPLICATION NUMBER: US/10/767,701
 CURRENT FILING DATE: 2004-01-29
 NUMBER OF SEQ ID NOS: 63128
 SEQ ID NO: 34787
 LENGTH: 138
 TYPE: PRT
 ORGANISM: Sorghum bicolor
 FEATURE: OTHER INFORMATION: Clone ID: SORBT-28MAY03-C54418_1_Pep
 US-10-767-701-34787

Query Match 10.5%; Score 97.5; DB 4; Length 138;
 Best Local Similarity 24.1%; Pred. No. 0.095; DB Matches 28; Conservative 26; Mismatches 57; Indels 5; Gaps 2; Length: 138; DB SEQ ID NO: 34787

Qy 27 GLDEEAIWRLSFTGIDDDT---MAALAAEQPLFEATADALVTDYHLESVERTQDLP 82
 Db 3 GMDKAEDAEPTCISSVQKETGHKYMADALEQODALIKKTKSLLVPSVLNHHDDIPGEADNY 62

Qy 83 ANSTKIVTEQKETQBYLLGLGRGEYDTEYAQQRARIGKIHVDVGLGPPVYLGAT 138
 Db 63 MDAINTLSESETESFQT-KNQEVPPAPSFNAEAQPVQAGAIDNIVQCPUSVYADFT 117

RESULT 3
 Sequence 18563, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIORITY APPLICATION NUMBER: US 60/360,039
 PRIORITY FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO: 18563
 LENGTH: 883
 TYPE: PRT
 ORGANISM: Halobacterium sp. NRC-1
 US-10-369-493-18563

Query Match 10.1%; Score 94; DB 4; Length 218;
 Best Local Similarity 28.7%; Pred. No. 0.39; DB Matches 47; Conservative 22; Mismatches 73; Indels 22; Gaps 8; Length: 218; DB SEQ ID NO: 9281

Qy 21 ALADRGIDBEI--AWRISF-TGIDDDTMALAAEQPLFEATADALVTDYHLESYER 77
 Db 25 ALADRGIVAHAEVFDVGRSLVASGVPEPVVKALUSGRPAGEPDQA--RFLQRIDLRR 81

Qy 78 TQDLFANSTKIVTEQKETQBYLLGLGRGEYDTEYAQQRARIGKIH--VGL 128
 Db 82 TR-LKPNRRYTYQEBIADGAGMSRQAGALIN-GDRRPTMEHCDAIQFRPRVHAGFLAE 139

Qy 129 GPDVVLGAVVRYYIGLDDALADVVADREBEEAAAVDELVAFL 172
 Db 140 DPEALAGTQLRSEOBILQQL---ADRRAAAMAVDDPLERL 178

RESULT 5
 Sequence 1480, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAMIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIORITY APPLICATION NUMBER: JP 2001-204089
 PRIORITY FILING DATE: 2001-05-30
 PRIORITY APPLICATION NUMBER: JP 2001-272697
 PRIORITY FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO: 13480
 LENGTH: 400
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-13480

Query Match 9.6%; Score 89.5; DB 4; Length 400;
 Best Local Similarity 26.7%; Pred. No. 2.5; DB Matches 36; Conservative 16; Mismatches 66; Indels 17; Gaps 5; Length: 400; DB SEQ ID NO: 13480

Qy 63 ALVTDYDYLSEYRTQDLPANSTKIVTEQKETQBYLLGLGRGEYDTEYAQQRARIGKIH--- 117
 Db 180 DVKSNEVQEGDRLADQIA--DKEADPHORLASHNTALAEVTADEHFEAEERQRQTRD 237
 Qy 63 ALVTDYDYLSEYRTQDLPANSTKIVTEQKETQBYLLGLGRGEYDTEYAQQRARIGKIH--- 117
 Db 238 ---DADAVLERYEBSRTALADVEETIADREAVEA-----AERETELADRVSNDHRE 286
 Qy 118 RICKHIDV-----LGL-GPDVVLGAVVRYTGLDAD--DVADRGEEAAAVDEL 167
 Db 287 RASDLDDEAAALAADLGDDPDBDASAER-----DAVADQREBAVAVREFAVAVRL 340

RESULT 4
 Sequence 9281, Application US/10156761
 US-10-156-761-9281

RESULT 6
 US-10-732-923-10618
 ; Sequence 10618, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIORITY APPLICATION NUMBER: 10/310,154
 ; PRIORITY FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO: 10618
 ; LENGTH: 400
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis MA-4680
 US-10-732-923-10618

Query Match 9.6%; Score 89.5; DB 5; Length 400;
 Best Local Similarity 26.7%; Pred. No. 2.5; Mismatches 66; Indels 17; Gaps 5;
 Matches 36; Conservative 16; Mismatches 66; Indels 17; Gaps 5;

Qy 42 IIDDMMALAAEQLPFEATADALVTDVFDHLEY-ERTQDLEANSKTKVEQLKETQAEY 99
 Db 2 LSEQSAATWTRATPIAVGAAGVETARFYDRLFARPEPLRDFNNG---NQAGTQROA 57
 Qy 100 LIG-G-LGRGEYDTEYAAQRA---RICKHDVIGLGDPDVYLGAYTRYVTGILDALADDV 152
 Db 58 LAGSIAAFATYLVEHPDAMDRLTAKHSLGIAFGQAYVHEDIFPAIAEVGDAY 117

RESULT 7
 US-10-282-122A-66025
 ; Sequence 66025, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Malon, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA-034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIORITY APPLICATION NUMBER: 60/191,078
 ; PRIORITY FILING DATE: 2000-03-21
 ; PRIORITY APPLICATION NUMBER: 60/206,848
 ; PRIORITY FILING DATE: 2000-05-23
 ; PRIORITY APPLICATION NUMBER: 60/207,727
 ; PRIORITY FILING DATE: 2000-05-26
 ; PRIORITY APPLICATION NUMBER: 60/230,335
 ; PRIORITY FILING DATE: 2000-11-27
 ; PRIORITY APPLICATION NUMBER: 60/257,931
 ; PRIORITY FILING DATE: 2000-12-22
 ; PRIORITY APPLICATION NUMBER: 60/267,636
 ; PRIORITY FILING DATE: 2001-02-09
 ; PRIORITY APPLICATION NUMBER: 60/269,308
 ; PRIORITY FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 66025
 ; LENGTH: 505
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis

US-10-282-122A-66025

Query Match 9.4%; Score 88; DB 4; Length 505;
 Best Local Similarity 25.7%; Pred. No. 4.8; Mismatches 69; Indels 40; Gaps 7;
 Matches 46; Conservative 24; Mismatches 58; Indels 40; Gaps 7;

Qy 6 DTLVTAIVRNGDGHALADRIGLDEEEIATWLSF---TGIDDDTMALAAEQPLF--- 57
 Db 325 DQALALAGRGGRGONVRLLASDQG-----WOLNIMTSAEDERNAAEDAAIRLFDMDHLN 377
 Qy 58 --BATADALVTDVFDHLE--SYERTQDLPFANSKTKVEQLKETQAEYILGLGRGEYDTEY 113
 Db 378 VBBETAVLVLDEGFATFEEVATVAPELLA---IBGFDDEBIVDMRNRAKDALTMAI 432
 Qy 114 AQPARIKHDV---GLGDPDVYLGAYTRYVTGILDALADDVADGEAAAVDELV 168
 Db 433 AAEKLGSEVSDDMRNLEGIDAD-----MRSLABAGITTRDDLAELAVDELLI 479

RESULT 8
 US-10-282-122A-65364
 ; Sequence 65364, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA-034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIORITY APPLICATION NUMBER: 60/191,078
 ; PRIORITY FILING DATE: 2000-03-21
 ; PRIORITY APPLICATION NUMBER: 60/206,848
 ; PRIORITY FILING DATE: 2000-05-23
 ; PRIORITY APPLICATION NUMBER: 60/207,727
 ; PRIORITY FILING DATE: 2000-05-26
 ; PRIORITY APPLICATION NUMBER: 60/230,335
 ; PRIORITY FILING DATE: 2000-11-27
 ; PRIORITY APPLICATION NUMBER: 60/257,931
 ; PRIORITY FILING DATE: 2000-09-06
 ; PRIORITY APPLICATION NUMBER: 60/230,347
 ; PRIORITY FILING DATE: 2000-09-09

PRIMER APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-11-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 65,664
 LENGTH: 496
 TYPE: PRT
 ORGANISM: *Neisseria gonorrhoeae*
 US-10-282-122A-65364
 Query Match Similarity 9.3%; Score 87; DB 4; Length 496;
 Best Local Similarity 25.7%; Pred. No. 5.9%; Mismatches 69; Indels 40; Gaps 7;
 Matches 46; Conservative 24; Mismatches 69; Indels 40; Gaps 7;
 QY 6 DLTIVLTAVRNGIDGHALADRGIDLEBIANWLSF--TGIDDDTMALAABOPLF---- 57
 Db 316 DRLALAGTGRGGCNRVRLASDLTG-----WQINIMTSAEADERNAAEDAATRRLFNMHN 368
 QY 58 -EATADALVDFYDILE- SYERTQDIFANSKTKVQLKTOAEYLGLGRGEDETEYA 113
 Db 369 VDEETADVLVQFGATEEVVAPBLLA----TEGDEBEIVDMLRNRAIDLITMAI 423
 QY 114 AQRARIGKIHDLV---GLGDPVLYGAYTRYTGLDADDVADRGEEAAVDELV 168
 Db 424 AAEKLGEGVSDMRNLEGVADML-----SLABAGITRDDLALAEVDEL 470
 RESULT 9
 US-10-848-111-14
 Sequence 14, Application US/10848111
 Publication No. US20040235107A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosenberg, Eugene
 ; APPLICANT: Ron, Eliora
 ; APPLICANT: Orr, Blisha
 ; APPLICANT: Paitan, Yossi
 ; TITLE OF INVENTION: GENE CLUSTER
 ; FILE REFERENCE: 27757
 ; CURRENT APPLICATION NUMBER: US/10/848,111
 ; CURRENT FILING DATE: 2004-05-19
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 14
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: *Myxococcus xanthus*
 ; US-10-848-111-14
 Query Match 9.3%; Score 86.5; DB 5; Length 318;
 Best Local Similarity 26.4%; Pred. No. 3.7; Mismatches 55; Indels 25; Gaps 3;
 Matches 34; Conservative 20; Mismatches 55; Indels 25; Gaps 3;
 QY 73 ESYERTQDIFANSKTKVQLKTOAEYLGLGRGEDETEYAQRARIGKIHDL---- 126
 Db 22 QSYFMKALELPQTGFRQRLDEQPKQRQHHSILERIYDARAARLDPDDVLSFPAI 81
 QY 127 -----GLGRDVYAGAYTRYTGLDADDVADRGEEAAVDELVAREL 172
 Db 82 PMIEHALRLIDRGIQPDAVVAGSMGEVALA-AIGAISVDAVALVAQAOLFARTA 139
 QY 173 P---MUKL 178
 Db 140 PRGGMIAVL 148
 ;
 RESULT 10
 US-10-437-963-137315
 Sequence 137315, Application US/10437963
 Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 137315
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: *Oryza sativa*
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_3880C.1.pep
 ; US-10-437-963-137315
 Query Match Similarity 9.2%; Score 86; DB 4; Length 362;
 Best Local Similarity 26.4%; Pred. No. 5; Mismatches 78; Indels 44; Gaps 9;
 Matches 51; Conservative 20; Mismatches 78; Indels 44; Gaps 9;
 QY 8 LVTADVNRNGIDGHALADRGIDLEBIAWR---LSFT---GIDDITMALAEEQPLFEATA 61
 Db 26 ILAABESTGTGKRLAS-IGVNEENRRALELFATGALDCLSGVILFEETLYQSTR 84
 QY 62 DALVDFYDILESY-----BRTQDIFANSKTKVQLKTOAEYLGLGRGEDETEY 112
 Db 85 DG---TPFVDSLAAAGVLAGIVKVDKGTVLAGTDRETTGHD-----GLGERCRRY 133
 QY 113 AQRARIGKIHDLVGLG-----PPDVLGAYTRY---YTGLDADDVAD-- 155
 Db 134 YAAGRFKURAVLSSIGRASSRPSQLOVANADQSLARYAIIQCENGIVPVERBILVGE 193
 QY 156 RGEAAAADVDELV 168
 Db 194 HGIEACEAVERV 206
 ;
 RESULT 11
 US-10-282-122A-66108
 ; Sequence 66108, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Olsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forbush, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: BLITRA.03A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848


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; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO: 11335
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
; US-10-156-761-11335

; Query Match 8.9%; Score 83.5; DB 4; Length 258;
; Best Local Similarity 24.1%; Pred. No. 5.7;
; Matches 49; Conservative 21; Mismatches 78; Indels 55; Gaps 9;
; Query 8 LVTADVRNGICHALADRIGDEAETAWRLSFTGIDDMMALAAEOPLFETADALVTD 67
; Db 33 WVVADVVLDD-QGEALAKEIGARYVHID---VGRDDWQAV-----TVAKD 74
; Qy 68 FVDHLESYE---RTQDLFANSTKTVEQKE-TQAEYLIGLGRGEYDTEYAOBARIG 120
; Db 75 AYGHIDGLVNNGAGILRNDLQGTPLAQFQQTIVQVNQVQVNFQIKTVAPEBE-AAGGTIV 133
; Qy 121 KHDVQIGLGPPVYLGAVT-----RVTGGLD-ALADDWA 154
; Db 134 NTASYAGLTGKAYVGAVYATTHAIVGGLTRVALELAALKRVRNAVCPGAIIDTAMSNPSQL 193
; Qy 155 DRG--BAAAVDELVARFIPM 174
; Db 194 DPGADPEETARALSELVGRVPL 216

RESULT 15
US-10-22-122A-59961
; Sequence 59961, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forborth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: E11TRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 59961
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-10-282-122A-59961

; Query Match 8.9%; Score 83.5; DB 4; Length 315;
; Best Local Similarity 25.4%; Pred. No. 7.4;
; Matches 51; Conservative 17; Mismatches 72; Indels 61; Gaps 9;
; Query 14 RNGICGHALADRIGDEAETAWRLSFTGIDDMMALAAEOPLFETADALV 65
; Db 116 RRNIDQVVLQFGFTGIDEMALPWR-----DTIVLMDARPGFASVQYDDEAITALM 167
; Qy 66 TDFYBH-----LESVRTDOLFANSTKTVQFOLKETOAEYLIGLGRGEYDTE 111
; Db 168 QRLYDRGRHITSFLGVPPVHSVDTTGERRHLAYLAFCKK-HRLIPTAALPGLGKOG-YDVT 225
; Qy 112 YAAQRARIKGK---HDVILGQPDVYLGAVYRYVYQGLDAD----- 148
; Db 226 ASVLTAAETSALVCATDTLALGASKYLQQCR-----DALQLASVGSTPLMKFLHPEILT 279
; Qy 149 ADDVVAADRGEEAAAVDELVA 169
; Db 280 VDPGVAESGRRAARQDIEQIA 300

Search completed: November 23, 2005, 05:09:02
Job time : 61.1486 secs

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QY 294 ATMTDIDEATDGVTAGVQLEGERAADVSVTGVGIDDI-AEQTNML--ALVANIEAARG- 349
 Db 244 TTNQAVQDEAKANAAEAAINAVIPIPKVVKQAAKDEBIDOLQATQNTNVINDQNTTEKEAAI 303
 QY 350 -----EAEFGFVVADE-----VKAEEESRE--STRVE 377
 Db 304 QOLATAVTDQKNTITATDDNGVQDQAKDAGHNSIOSTQPATAVSKNAKNDVQDQVTONQ 363
 QY 378 ELVEQMQAEETETVVDOLDEV-----NORIGEGERV-EBAMETIQTETT-DAV 422
 Db 364 AIDNTGATTEKNAKDLYKAKEAYQDILNAQTNNDVQDQAVADIGTADTTI 423
 QY 423 EDASGMOEVSTATDQQA-----VSTERVAEMWDGV-----DRAGETAAULDIA 468
 Db 424 KDVAK--DELTAKANEOKALIAQTADATTEKEQANQVDAQLTQGNQNIENAQSDDVN 481
 QY 469 DATDQVRTVVEVR 482
 Db 482 TAKDNQIAQIDPIQ 495

RESULT 2
 US-10-984-376-5
 Sequence 5, Application US/10984376
 Publication No. US2005024436A1
 GENERAL INFORMATION:
 APPLICANT: GIULIANI, Marzia Monica
 APPLICANT: PIZZA, Mariagrazia
 APPLICANT: RAPPOLI, Rino
 TITLE OF INVENTION: COMBINATION NEISSERIAL COMPOSITIONS
 FILE REFERENCE: 2300-1609.20
 CURRENT APPLICATION NUMBER: US/10/984,376
 PRIOR APPLICATION NUMBER: 09/979,263
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: PCT/IB00/00828
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: GB 9911692.3
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: GB 0005730.7
 PRIOR FILING DATE: 1999-08-19
 PRIOR APPLICATION NUMBER: GB 0005730.7
 PRIOR FILING DATE: 2000-03-09
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 6
 LENGTH: 364
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: representative ORF 961 protein
 US-10-984-376-6
 Query Match 6.7%; Score 160; DB 1; Length 364;
 Best Local Similarity 23.5%; Pred. No. 0.0058; Mismatches 11; Indels 54; Gaps 11;
 Matches 67; Conservative 45; Mismatches 11; Indels 54; Gaps 11;
 QY 236 MRARTDDQVORMADVS-----REISSV/SASYEVVASTPADDERRRTSDEAALAQGEA 287
 Db 24 LAATSDDDVKKATVAIVAAVNNGQEEFNGKAG-BTIVDGEDGTQDQA----ADV 78
 QY 288 ADD-----ALATMT-----DIDEATDGVTAGVQLEGERAADVSVTGVGIDIA 331
 Db 79 EADDFKGIGLKVKVWTNLTKTWNENKQNDKVKAAESELKLTKLADTDALADTDAL 138
 QY 332 BOTNMALANIASTEARAGAEAGEGFVVADEVKALABEESRQSTROVREVBVEQMOAETETV 391
 Db 139 DETTN-ALN-----KLEGENITTAFAETTKNIVKIDEKLEAVADTVDKHAFAFDIA 188
 QY 392 DQDDEYNQRGEGVERVEREAMETIQTETDVE-----DASGMOEVSTATDQAVSTEE 445
 Db 189 DSDLENTKADBAVKTAEAKTQDQETKQNDKVKAAETAGKAACTANTRDAE 248
 QY 446 VAEMWDGVDDRAGEAALDDIA-----DATDQVRTV-EEVRE 483
 Db 249 A--VAAKVTDIKADATKNAKDIANSARTDSLKNVANLRKETRO 291

RESULT 4
 US-10-793-626-3188
 Sequence 3188, Application US/10793626
 Publication No. US20050255478A1
 GENERAL INFORMATION:
 APPLICANT: KIMMELLY, WILLIAM JOHN
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERmidis NUCLEIC ACIDS AND PROTEINS
 FILE REFERENCE: PUS3480US
 CURRENT APPLICATION NUMBER: US/10/979,626
 CURRENT FILING DATE: 2004-03-04

FILE REFERENCE: 821A ;
; CURRENT APPLICATION NUMBER: US/10/821, 234 ;
; CURRENT FILING DATE: 2004-04-07 ;
; PRIORITY APPLICATION NUMBER: US 60/1462, 047 ;
; PRIORITY FILING DATE: 2003-04-07 ;
; NUMBER OF SEQ ID NOS: 1704 ;
; SOFTWARE: pt SEQ_genes Version 1.0 ;
; SEQ ID NO 1477 ;
; LENGTH: 667 ;
; TYPE: PRT ;
; ORGANISM: Homo sapiens ;
; US-10-821-234-1477 ;

Query Match 6.0%; Score 142.5; DB 1; Length 667;
Best Local Similarity 19.4%; Pred. No. 0.098; Mismatches 186; Indels 143; Gaps 19;
Matches 97; Conservative 75; MisMatches 186; Indels 143; Gaps 19;

Qy 53 EQQLFEATADALVDFYDYLESYERTQDILFANSTKTVQLEKQAE-YLLGGRGEDE 111
104 DKPGSKSGMDAALDDLDITLGGBETEE-ENTYTGFPEVSDPMSSYIEBLGKREV-TI 160
Qy 112 YAQRARIGKTHWLG-----LGPPWYLGATRYVTGLLQALADD-----VWADRG 157
161 PPKYRELAKKEGTGPPADSKPPIGP-----DaidalissptcsptaaGK 209
Db 158 BAAAAVADLVARFLPMLKLTFFQQ---IAMDITYISYAQRARIGKTHWLG-----VADLWADRG 213
Qy 210 TEKEESTEVIAKQASGTVRSAAQPKERKVEKDMSQDALEALASLHGTR 262
Db 214 HVEAPLSSIEATSDQVAEPTDWTMARTDQ-----VIR---MADVREISSVS 258
263 EPELDLRSIKEVDEAKAKEKLEKCGEDDETIPSEYRUKPATDKGKPLPFEKKPR 322
Qy 259 ASVEEVASTADDYRTSEAAEALAAQGQBAADDALATWMDIDAT----- 303
Db 323 SESELIDELSEDFDR-SECKEKPSPKTEKESKAAPAPVSEAVCRSMCSIQSAPP 381
Qy 304 -----DGTVACGEQLEGERAADVESVTGVIDIAEQTNMLANASIEAARGAGEG 354
382 ATLGKGTVPDDAELADSLGKKEADPDKPVMUKVEKAK----- 422
Db 355 FAVVADDEVKALAAESEQESTRVEELVOMQAETETV-----QDDEVNGIGEV-----ERVE 409
423 -----EEDEK-----LGEKSETIPDYRLBEVKOKDGKPLPKSK 459
Qy 410 EAMETLQE-ITDAVEDAASGMQEVTSTADEQ---AVSPEVAMWDGVDDRAG----- 458
Db 450 EQLPPMSEDFLDALEDFSGPQNASSKLPEDAKLAIASEEVNSQTPASTTQAGAPPDT 519
Qy 459 -----EIAALDDIADATDQ 474
Db 520 SQSDKDDDAKLDKLPSIGR 540

RESULT 9
US-11-074-176-80
; Sequence 80 Application US/11/074-176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAluliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Thereof
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; PRIORITY APPLICATION NUMBER: GB 0118825.9
; CURRENT FILING DATE: 2004-02-02
; PRIORITY FILING DATE: 2001-08-02
; PRIORITY APPLICATION NUMBER: GB 0200349.9
; PRIORITY FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Staphylococcus aureus ;
; US-10-485-517-146

Query Match 5.9%; Score 141; DB 1; Length 706;

Best Local Similarity 19.4%; Pred. No. 0.13; Mismatches 218; Indels 122; Gaps 23; Matches 105; Conservative 96; Mismatches 218; Indels 122; Gaps 23; Score 140.5; DB 1; Length 989; Query Match 5.9%; Score 139.5; DB 1; Length 1586; Best Local Similarity 18.6%; Pred. No. 0.19; Matches 113; Conservative 122; Mismatches 219; Indels 153; Gaps 27; Prior Application Number: US 60/462,047

Qy 5 5 NTPLVTADVRGIDGHA-LAIGLGBEABIAWRLSFRGIDDDTMALAAEOPLFENTADA 63

Db 336 SDSTIGADSLLIDISBADDQDLSLILQAKVA---SLTHINKELODKLAQKSP-BAEADL 391

Qy 64 LVTDFYDHLBSYERQ-DLFANSTKTE---QKETQAELYLIGRGRGYDTE-AAQRAR 118

Db 392 -----SFDSYHSTQTDLPGSPLSKGPGTSPPDKSSPSVLHSILGSTTDND---VR 439

Qy 119 IKIKHDVUGLGPDV-----YLGAVTRYTGILDALADDVADVRGEERAANADE 166

Db 440 IQQLQBL---QDUQKRLLESSEARPKQLOVELQRRRAELVCLNNTTEISNNSDLSOKLKE 496

Db 87 LAGSPTVEQINTNTSTANQAKSDL-DHARQALTPDKAPLQTAKT--OLEQSINQPDITG 143

Qy 100 L1GLGGEYDDEYAAQARIKHDVIGLGLDPWYLGATRYTGILDALADWDVDRGEE 159

Db 144 MTTASLNAVYQKLOAQRKLTBINOVINGNTR-----QNTINDKUTE 185

Qy 160 AQAQAVEL-VARFLPMLKLTFDQQIAMDWTIDSYAQLRHIBIDSQ-----ELANAV 211

Db 186 ANAQAKQQLNTAR---QSLIDLDRQPAUT-----LHGSANINAQQAQNFTQINA 232

Qy 212 ATH----VEAPLSSLEA-----TSQDVARTDTWARTDQVDRMADV 250

Db 233 QNHAALETIKVNTAINTMTKLDSVADNNTIKSDSNTYATPANKQAYDNAAWAKV 292

Qy 251 SREISSLSSASVEVASTADDYRRTSE--DAAALQCEAADDALATMIDDEATDGYA 308

Db 293 IGETTNPTMDNTVNQKASVYKSTKQALDQGONLQRKTEATNAITHASDINAQKN--- 349

Qy 309 GVEQLGERAADEVSVTQVGDIDTAEQTMNLJANASIEARAGERGEAEVVADE-VKALAE 367

Db 350 ALTOQVNSAQNOVAQ---NPKQKTO--SNTAMGTLKRRVANHNOVYQVSDNQYADTN 403

Db 368 ESREQSTRVELVEQMQAETEETVDQDLEBUNRIGEERVERBEAMETLOETDAVEDAAS 427

Qy 404 KGDYNNAYNHANDINGNAQHVPITSDVNNA-SVNTSEHALNEAKUNAKOANT 462

Qy 428 GNOEVSTATDQAVSTEEV--AEMUDGVD--DRAGEIAALDDI--ADTDQORTVE 479

Db 463 ALGHLNNLNNAQRNQLOSQINGAHQIDAINTKQNATNLNSAMGNLRQAVADKDKQVRTE 522

Qy 480 E 480

Db 523 D 523

RESULT 11

US-10-821-234-975

; Sequence 975, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821, 234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: PC_SEQ_genes Version 1.0

; SEQ ID NO: 975

; LENGTH: 989

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-975

Query Match 5.9%; Score 140.5; DB 1; Length 989; Best Local Similarity 18.6%; Pred. No. 0.19; Matches 113; Conservative 122; Mismatches 219; Indels 153; Gaps 27; Prior Application Number: US 60/462,047

Qy 5 5 NTPLVTADVRGIDGHA-LAIGLGBEABIAWRLSFRGIDDDTMALAAEOPLFENTADA 63

Db 36 SDSTIGADSLLIDISBADDQDLSLILQAKVA---SLTHINKELODKLAQKSP-BAEADL 391

Qy 64 LVTDFYDHLBSYERQ-DLFANSTKTE---QKETQAELYLIGRGRGYDTE-AAQRAR 118

Db 392 -----SFDSYHSTQTDLPGSPLSKGPGTSPPDKSSPSVLHSILGSTTDND---VR 439

Qy 119 IKIKHDVUGLGPDV-----YLGAVTRYTGILDALADDVADVRGEERAANADE 166

Db 440 IQQLQBL---QDUQKRLLESSEARPKQLOVELQRRRAELVCLNNTTEISNNSDLSOKLKE 496

Db 87 LAGSPTVEQINTNTSTANQAKSDL-DHARQALTPDKAPLQTAKT--OLEQSINQPDITG 143

Qy 100 L1GLGGEYDDEYAAQARIKHDVIGLGLDPWYLGATRYTGILDALADWDVDRGEE 159

Db 144 MTTASLNAVYQKLOAQRKLTBINOVINGNTR-----QNTINDKUTE 185

Qy 160 AQAQAVEL-VARFLPMLKLTFDQQIAMDWTIDSYAQLRHIBIDSQ-----ELANAV 211

Db 186 ANAQAKQQLNTAR---QSLIDLDRQPAUT-----LHGSANINAQQAQNFTQINA 232

Qy 212 ATH----VEAPLSSLEA-----TSQDVARTDTWARTDQVDRMADV 250

Db 233 QNHAALETIKVNTAINTMTKLDSVADNNTIKSDSNTYATPANKQAYDNAAWAKV 292

Qy 251 SREISSLSSASVEVASTADDYRRTSE--DAAALQCEAADDALATMIDDEATDGYA 308

Db 293 IGETTNPTMDNTVNQKASVYKSTKQALDQGONLQRKTEATNAITHASDINAQKN--- 349

Qy 309 GVEQLGERAADEVSVTQVGDIDTAEQTMNLJANASIEARAGERGEAEVVADE-VKALAE 367

Db 350 ALTOQVNSAQNOVAQ---NPKQKTO--SNTAMGTLKRRVANHNOVYQVSDNQYADTN 403

Qy 368 ESREQSTRVELVEQMQAETEETVDQDLEBUNRIGEERVERBEAMETLOETDAVEDAAS 427

Db 404 KGDYNNAYNHANDINGNAQHVPITSDVNNA-SVNTSEHALNEAKUNAKOANT 462

Qy 428 GNOEVSTATDQAVSTEEV--AEMUDGVD--DRAGEIAALDDI--ADTDQORTVE 479

Db 463 ALGHLNNLNNAQRNQLOSQINGAHQIDAINTKQNATNLNSAMGNLRQAVADKDKQVRTE 522

Qy 480 E 480

Db 523 D 523

RESULT 12

US-10-821-234-901

; Sequence 901, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821, 234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704

; SOFTWARE: PC_SEQ_genes Version 1.0

; SEQ ID NO: 901

; LENGTH: 1586

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-901

Query Match 5.9%; Score 139.5; DB 1; Length 1586; Best Local Similarity 20.3%; Pred. No. 0.37; Matches 90; Conservative 99; Mismatches 183; Indels 99; Gaps 15; Prior Application Number: US 60/462,047

Qy 83 ANSTKVEQLEKTOEYLGLGR---GEYDTEYAAQARIGKHDVIGLGLDPWYLGAY 137

Db 915 AGEAKVKQLOVAREQEBITAVQARMQASYREHVKEVQQLQCKIRTLOEQLENGPNTQARL 974

Search completed: November 23, 2005, 05:09:26
Job time : 17.766 secB

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 23, 2005, 04:37:11 ; Search time 47.9554 Seconds
(without alignment)
843.041 Million cell updates/sec

Title: US-09-455-978B-2
Perfect score: 2394
Sequence: 1 MSNDNDLTVLADVRNGIDGH..... ATDQQVRTVEEVREBTVGKLS 489

Scoring table: BL05M62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued Patents RA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	412.5	17.2	640	2	US-09-252-991A-23252		Sequence 23252, A
2	401.5	16.8	545	2	US-09-252-991A-31086		Sequence 31086, A
3	398	16.6	663	2	US-09-252-991A-23255		Sequence 23255, A
4	397.5	16.6	906	2	US-09-252-991A-32715		Sequence 32715, A
5	389.5	16.3	696	2	US-09-252-991A-16965		Sequence 16965, A
6	388.5	16.2	897	2	US-09-252-991A-15636		Sequence 15636, A
7	385	16.1	710	2	US-09-252-991A-3289		Sequence 32789, A
8	380.5	15.9	734	2	US-09-252-991A-30703		Sequence 30703, A
9	380.5	15.9	857	2	US-09-252-991A-23956		Sequence 23956, A
10	379	15.8	701	2	US-09-252-991A-2288		Sequence 2288, A
11	373.5	15.6	709	2	US-09-328-352-5172		Sequence 5172, AP
12	373	15.6	614	2	US-09-252-991A-31412		Sequence 31412, AP
13	368.5	15.4	573	2	US-09-252-991A-18744		Sequence 18744, A
14	366	15.3	760	2	US-09-252-991A-31724		Sequence 31724, A
15	361	15.1	613	2	US-09-252-991A-25899		Sequence 25899, A
16	360	15.0	520	2	US-09-902-540-14226		Sequence 14226, A
17	359	15.0	579	2	US-09-543-681A-6665		Sequence 6665, AP
18	358.5	15.0	611	2	US-09-252-991A-20097		Sequence 20097, AP
19	352.5	14.7	563	2	US-09-252-991A-31048		Sequence 31048, A
20	350.5	14.6	521	2	US-09-902-540-1865		Sequence 1865, A
21	349	14.6	487	2	US-09-902-540-14739		Sequence 14739, A
22	349	14.6	510	2	US-09-902-540-15074		Sequence 15074, A
23	348.5	14.6	684	2	US-09-252-991A-28604		Sequence 28604, A
24	347	14.5	547	2	US-09-902-540-16229		Sequence 16229, A
25	346.5	14.5	504	2	US-09-252-991A-26180		Sequence 26180, A
26	343.5	14.3	537	2	US-09-252-991A-20929		Sequence 20929, A
27	343.5	14.0	653	2	US-09-252-991A-18264		Sequence 18264, A

ALIGNMENTS

RESULT 1
US-09-252-991A-23252
; Sequence 23252, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196_136
; CURRENT APPLICATION NUMBER: US/09-252-991A
; CURRENT FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 90
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23252
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23252

Query Match 17.2%; Score 412.5; DB 2; Length 640;
Best Local Similarity 24.4%; Pred. No. 1.1e-24;
Matches 149; Conservative 97; Mismatches 199; Indels 165; Gaps 19;
Sequence 31086, A
Sequence 23255, A
Sequence 23255, A
Sequence 32715, A
Sequence 16965, A
Sequence 15636, A
Sequence 32789, A
Sequence 30703, A
Sequence 23956, A
Sequence 2288, A
Sequence 5172, AP
Sequence 31412, AP
Sequence 18744, A
Sequence 31724, A
Sequence 25899, A
Sequence 14226, A
Sequence 6665, AP
Sequence 20097, AP
Sequence 31048, A
Sequence 1865, A
Sequence 14739, A
Sequence 15074, A
Sequence 28604, A
Sequence 16229, A
Sequence 26180, A
Sequence 20929, A
Sequence 18264, A
Sequence 16229, A
Sequence 224 LKTLABAYPKGAPNIVPGVHEVLDGRSQFVSTPVKGLPGVTVWYALVLDRTAYMSL
Db 104 SRNFASVVLGEAASGTFMRPYDAMPGSDPRTRWYKDALAADDLTVTERFDAGTCQ
Db 164 ILAMSLPVKHAGQLGVANGDMKLETITAILNSLKFGAYARLVSQDGKILJHPDGLV
Qy 58 -----ATADALVTFDHL-ESYE-KTQDILANS-----TKTVEQ 91
Qy 7 TLYTADLVNGIDG----HALADRIG----BAAEIRWLSFTGIDDTMAAABEGPLF 57
Db 59 TLATNTQSWLGRMHMLVLEGASOLALDQDPAEANIAQL-----E(P)PFV 103
Qy 92 -----LKEQDAEYVLGLGSGEYDTE-----YQAQRARIKI--HDVGL- 128
Qy 164 ILAMSLPVKHAGQLGVANGDMKLETITAILNSLKFGAYARLVSQDGKILJHPDGLV 223
Qy 129 -----GPDVYGLR-----TRYVGLD----- 146
Db 224 LKTLABAYPKGAPNIVPGVHEVLDGRSQFVSTPVKGLPGVTVWYALVLDRTAYMSL 283
Qy 147 -----AlLADWVA-----DRG--EEAAAVBLVAPFLPMKL 178
Db 284 BFRTSIAVATLIAVVGIMLLGMLIRVMQPLDMGRAMQDGEGLTRK---LKVT 339
Qy 179 TFDQOIAMDTYISYQAQLHEDDSRQBLANAVATHBAPLSSLEANSQDVAERTDTMRA 238
Db 340 SNDRFTGLANAFNRFVERHEST--REVAGTA-----RQHDAQLVNTASNSMA 388

QY 239 RTDDQDVDRMAYVSRETSVSVASVEEVASTADDVRRTSEDAEALAOQGEAADDALATM 298
 Db 389 NSDEQSNRTNSVAAINELGAQAEIARNADASHASDANHQADGKQVETIRANNE 448
 QY 299 IDEATGVTAGVEOLGERAAADEVSFVGVGVIDAETQNMALANASIEARAGEAERGFV 358
 Db 449 ISEKUSASCANIEALNSRTVNGQILEVKIGISEQTNLALNAAIEARAGEAERGFV 508
 QY 359 ADEVKAELAESREOSTRVEEVEQMAETETDQDVNVORIGSGVERVEAMETQEI 418
 Db 509 ADEVNLALHRAQESAOQIQMEELOQGAQAVSTWESORSYLESVEIANRAGERLGSV 568

RESULT 2
 US-09-252-991A-31086
 ; Sequence 31086, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094, 190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 31086
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-23255
 ; Query Match 16.8%; Score 401.5; DB 2; Length 545;
 ; Best Local Similarity 24.9%; Pred. No. 6.6e-24;
 ; Matches 131; Conservative 111; Mismatches 205; Indels 79; Gaps 16;
 ; QY 3 NMDNTLUTADPRTNGDGHALDRIGDEAEAWRLSPTGPIDDWTMALARQPLFETAD 62
 ; Db 47 SENELSYNA-LRNHMEGMDMD-----ALRADVLAFAFVV-OPGDGAEE 88
 ; QY 63 ALVTDVDHLSYERYTQDPLFANSTKVEQ----LKEHQARYLGLGRGEVTEYNAQRA 117
 ; Db 89 QYRQDQEHSPFR-----KUVEQNGPLDIAHQALVEL-RPDILEYIGAES 137
 ; QY 118 RIGK-IMDVLSGPDV--YLGAYTRYVTGLDALADD----VADRGEE----- 159
 ; Db 138 IVGKALLDPVARAELRQFVQAF-KELEGRIEALLSLIEKHEQTRAREDSMRVSAWML 196
 ; QY 160 -----AAAVDELVAPFL---PMKLKL-----TDDQIAMDTYDSYQWLHD 199
 ; Db 197 AGGILVACLVQGCOLCROLLRPLKVLVASARVIAQGNLQEPIGDS--DDEAQCLQR 254
 ; QY 200 EIDSRQELANAVATHVAPLSSLEAQDVAERTDTMRARPDQDQVRMADWSRELSVA 259
 ; Db 255 ALGEMDPLRMLPMTTIRQESBLHDPSQTSOSITSDVGSQADSATSAHSHEMIT 314

RESULT 3
 US-09-252-991A-23255
 ; Sequence 23255, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US 60/074, 788
 ; PRIOR APPLICATION NUMBER: US 60/094, 190
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 23255
 ; LENGTH: 663
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-23255
 ; Query Match 16.6%; Score 398; DB 2; Length 663;
 ; Best Local Similarity 28.3%; Pred. No. 1.6e-23;
 ; Matches 118; Conservative 74; Mismatches 171; Indels 54; Gaps 10;
 ; QY 103 LGRGRYDTEVAQARARIGKITHDVLGL-GPFDVIG-----AY---TRYTGIDLAD 151
 ; Db 261 IGSGSEAEHLG-NTRILSPSPVKGKLSGDWYIGISVSKDKAVMLTKURTSIAVALLA 319
 ; QY 152 VVA-----DRG---EELAAAVDELVAFPLPMKLUFLDQQIAMDTYID 191
 ; Db 320 VVATVLLGMLIRVLMQPLTDGMGRAMQDIAQGEGLTRR---LKVTSDNFGTLANAFN 375
 ; QY 192 SYAQDLHEDIDSQRLANAVATHTEAPLSSLEATSQDVAERTDTMRARPDQDQVRMADWS 251
 ; Db 376 RFVFLHESI---RIVAGTA-----RQLHDYAQLVNASHNSMMAISDEQSRNTSYA 424
 ; Db 312 QLGERAADVSFVGVIDIAETQNMALANASIEARAGEAERGFV 371
 ; QY 252 REISSVASSVEEVASTADDVRRTSEDAEALAOQGEAADDALATMIDDEATGVTASVE 311
 ; Db 425 AAINELGAAQAEIARNADASHASDANHQADGKQVETIRANNE 484
 ; QY 485 ALNSRTVNGQILEVKIGISEQTNLALNAAIEARAGEAERGFV 544
 ; QY 372 QSTRVEELVQMAETETDQDVNVORIGSGVERVEAMETQEIATDAEASGMQ 431
 ; Db 545 SAQQWMLTBLQIGAQAEISTMTEESORSYLESVEIANRAGERLGSVTCRAEDGMNOS 604
 ; QY 432 VSTADBEAVSTEEVAEMVGDVDRMAYVSRETSVSVASVEEVASTADDVRRTSEDAE 488
 ; Db 605 VATATEEOTA-----VVDSLNMDITEINTLNGEVENLQATLRCABELETQAGRL 654

RESULT 4
 US-09-252-991A-32715
 ; Sequence 32715, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107-96-136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 32715
 LENGTH: 906
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-32715
 Query Match 16.6%; Score 397.5; DB 2; Length 906;
 Best Local Similarity 24.8%; Pred. No. 2.8e-23;
 Matches 129; Conservative 87; Mismatches 158; Indels 147; Gaps 13;
 Qy 79 QDLFANSTKTVQEQLK-----ETQAEYLGLGRGYDTEAAQRARIKGKHDVGLGPD 131
 Db 406 QDLFNNRMKPKISQLKIVADAVAVSVVDALHKTRAGYFDEERLQELS----- 452
 Qy 132 VLYGATVTRYVGLDALLADYVADRCBEEAAAVDELVAREPLMLKL----- 178
 Db 453 ---GALRIEKSWADYSAD-----HRTAAKEKITESLVTPLRVRKRMFLAYGQARA 501
 Qy 179 -----TDDQI-----AMTYID---SYAQRLHDEIDSROE----- 206
 Db 502 GSLRNNTBAGTFRNREMGAFDPLGTLAISLIDQLQSGAKLNUQMEGRYDMSRTTFLIGA 561
 Qy 207 -----LAMAVATHEAPSSPLEATSQDAERTH-TMR---ARTDQV----- 244
 Db 562 AALVLVVAAWFISLIMPLSDLRGVIRRQDSSNLTRADGRDVESTDARAFNML 621
 Qy 245 -----DRMADVSRESSVSAS-----VESVASTADDVR 272
 Db 622 ESQQALRHLAETARKLUTITSBDEMSAISNOVSHVATSGQDQTMVAVTHOMSMAYQDV 681
 Qy 273 RTSEDAEALAOQGEAADDALATMWDIDEATGVT-----AGVBDOLGERAADVSVTG 325
 Db 682 RNAQAAASAAESANSANSAHTGTGIVHANLDAQGLSNWGEAGAVIOTRNKTEELSTVLE 741
 Qy 326 VIDDIASOTNMALAINASIAEARAGEGEGFAVADAEVYKALABESRFOSTRTEBLVQWQA 385
 Db 742 VIQNIAQOTNLALNAAIEAARAGEGEGFAVADEVRSLATNTKATEIREMIALQA 801
 RESULT 5
 US-09-252-991A-16965
 Sequence 16965, Application US/09252991A
 Patent No. 655175
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 16965
 LENGTH: 906
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-16965
 Query Match 16.3%; Score 389.5; DB 2; Length 696;
 Best Local Similarity 25.3%; Pred. No. 8.4e-23;
 Matches 131; Conservative 98; Mismatches 210; Indels 79; Gaps 14;
 Qy 1 MSNDUDLTVTADVRGIDGHALDRI---GIDEAELAWLISFTGDDDTMALLAABQPLFE 58
 Db 213 LAGDDENSVQAD-SFRGRDA-SLGRVLUKGMOEGBNAAMSISKY-TNAEAVDRLNELBFE 269
 Qy 59 ATADALVTDYDHLSYERQDLF-----ANSTKVEOLKETEYL---GLGRGEYD 109
 Db 270 ---FVSGSVD-ELETSPDLCFQREANNNTSVSQTLDKASQLDGCFENLAGRSI 322
 Qy 110 TEYAAQRARIGKIHVDLGLGRDVLYGATRYTYG----- 150
 Db 323 NLFA-----GYVGLALASILIGLVMRETNRLAETAEKURNOAIIRLUDBIA 376
 Qy 151 DVADRGEEAAAVELVARFLPMKLUITDQDQIAMDYTSYQARLHBDISROELA-- 208
 Db 377 -LADCDLTVAATVE----- 413
 Db 209 -NAVATHVEARLSSLEATSQDAERTDMARTDQDVRMADVSEISSVASEVAST 267
 Db 414 INQATQVAAQAAQETOSTAMHAE-----ASERQAQETAGASAIAENMAVISIDQVSAN 466
 Qy 268 ADDVRTSEDAEALAOQGEAADDALATMWDIDEATGVTAGVEOLGERAADVESVTGVI 327
 Db 467 AEESSAAVAAEVAIAKGNVEWNVHTGMUNREIQDTSKRIKKGESSQETIGDIVSLI 526
 Qy 328 DDIAEQTNMALLAINASIAEARAGEGEGFAVADAEVYKALABESRFOSTRTEBLVQWQAET 387
 Db 527 NDIAQDTNILLANIAIQASWAGDAGRGFAVADAEVORLABERSAAQTKIARVKTQDT 586
 Qy 388 EETDQDDEVNQRIGEYVVERVEAMTLOQITDAEVAASGMQEISTDEQAVSTEEVA 447
 Db 587 NEAVISMEQTSESVVRGARLAQDAGVALETEKVKSTLALQNTSNAARQOASSAGHIS 646
 Qy 448 ENVDGVDRAHGTRAAALDDADQDQVRTVEEVETV 485
 Db 647 NMVNVIQETTSQTSAGTTATRSIGNLAKMASMRNSV 684
 RESULT 6
 US-09-902-540-15636
 Sequence 15636, Application US/09902540
 Patent No. 6833447
 GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegand, Roger C.
 TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10(15849)B
 CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO: 15636
 LENGTH: 897
 TYPE: PRT
 ORGANISM: *Myxococcus xanthus*
 US-09-902-540-15636
 Query Match 16.2%; Score 388.5; DB 2; Length 897;
 Best Local Similarity 26.1%; Pred. No. 1.4e-22;
 Matches 132; Conservative 107; Mismatches 202; Indels 65; Gaps 15;

RESULT 9
US-09-252-991A-23956
Sequence 23956, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 23288
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23956
Query Match 15.9%; Score 380.5; DB 2; Length 857;
Best Local Similarity 26.8%; Pred. No. 5.9e-22;
Matches 141; Conservative 92; Mismatches 226; Indels 67; Gaps 16;
Matches 96; Conservative 67; Mismatches 146; Indels 22; Gaps 4;
Qy 2 SNNNDTLYTADYVRNGIDCHALADRIGD-----SEBIAN--RLSFTGIDD----DTM 47
Db 352 ANSLDITLQSSLADG--AYALKESQHGHDGEPPLQQAQVAQNRLVQGLGLDEARSLEAR 409
Qy 48 AALAAEQP--LFEA-----TADALYTDFYHLESVERTQDLFANSTKTKTEQLK 93
Db 410 AADAAQEGPKSLREALELAARLQEQATTDAYSVWKVOUTNRGFKLAE--YRASOLO 467
Qy 94 ETOAEYLIGLGRGE---YDTEVAQARARIGKTHDVGIGLGPDVYLAGVTRYTGLIDALA 149
Db 468 ERQWYAAMGERACQWMARVDRSWEAQOAM--LHS-LRTNSLILVGA----AVIALLV 518
Qy 150 DDVVAQDRGEEAAIAVDELVARFLPMKLTDFQDQIQA---MDTYIDSAYAQLRHDIEISRQE 206
Db 519 -----GLGAARGISLILVR--PLRQAMGAHRIAGEDLAVRVDs--ERRDEVGQMLA 566
Qy 207 LANAVATIVEAPLISLE-----ATSDQVAERTTDMARTDPDQVDRMADVREISSUSA 259
Db 567 AMGAMTGSLRGLIVSQLQPGVGRIGASEALSGVTRTRIGLISQSRATEQVATAMNGMAA 626
Qy 260 SVERVASTPADDVARTSEDAEALAQGEAADDALATMWDIDEATDGVTAGVOLGERAAD 319
Db 627 TVEREWAHRAEAGAAGAESADGKSVGQEVROTLERERLAEAVRATASVEALADSQR 686
Qy 320 VESVTGIVGIDIAFQDQTMALANASIEAARAGEAGEFAYVADAEVKALARESREOSTRVEEL 379
Db 687 IGSVLDVTKSVABOTNLQALNAAIEEARAGDQGRGFAVVADEVRALRRTQOSTATEBTL 746
Qy 380 VEQMQAEETETDOLDEVNQFQIGEGVERVEEAMETLQBTIDAVEADASGMQEVSTADEQ 439
Db 747 IGALQNGTQQAVQRMQSHOLVQDQSDQDQDQVTRVEVETTV 485
Qy 440 AVSTEVAEMDVGVDRAEIAAADDITADATDQOQVRTVEVETTV 806
Db 807 SAVAEINNSVTAIREVADQSAQAMOSTASSBOLAEGLGRELOQMM 852
RESULT 10
US-09-252-991A-23288
Sequence 23288, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 23288
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23288
Query Match 15.8%; Score 379; DB 2; Length 701;
Best Local Similarity 29.0%; Pred. No. 5.9e-22;
Matches 96; Conservative 67; Mismatches 146; Indels 22; Gaps 4;
Qy 158 EAAAIAVDELVRFPLMILKLTDDQDQIAMPDTIDSQAQRLHDEISROELANAVATHVEA 217
Db 384 QDIAQSEGDLTKR---LAVRSRDERGFGVGLDFAFNQFVERIHSI---REVAGTA----- 430
Qy 218 PLSSEATSDQVAERTDTMARTDDQDQVDRMADVREISSUSAVERVASTADVRRTSED 277
Db 431 --HKLHDVSLQVNNSMANNSMSDEQNSRNTNSVAAINELGAAQBLARNADASHD 488
Qy 278 AEAIAQGEAADDALATMWDIDEATDGVTAGVEOLGERAADVESTGIVDIDAEQTNML 337
Db 489 ANHQAEKGQVQEVTQTRMHNLEKISASCANIEALNSRNTVNGQILEVKIGISEQTNLL 548
Qy 338 ALNASTEARAGEAGECPAVDDEVKALESSERSQESTRVEELVEQMQAEETEFTQDLEV 397
Db 549 ALNATAEARAGEAGECPAVDDEVNLHRAESQAQIORMIEBLOVQAREAVATMTE 608
Qy 398 NORIGEGERVERVEAMETLQETIDAVEDAASGMQEVSTADEQAVSTEEVAAEMDGVDDRA 457
Db 609 QRYSLESVEIANRAGESLSVTRRIGEIDGMQNSVATATEEQTA-----WVDISLMDI 661
Qy 458 GIAAALDDIADATDQVRTVEFRETFVGKL 488
Db 662 THINTLNQEGVNLQATLRCACBETQAOGRIL 692
RESULT 11
US-09-328-352-5172
Sequence 5172, Application US/09328352
; Patent No. 6552958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACTINETOBACTER
; TITLE OF INVENTION: BAINMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO: 5172
; LENGTH: 709
; TYPE: PRT
; ORGANISM: Actinetobacter baumannii
; US-09-328-352-5172
Query Match 15.6%; Score 373.5; DB 2; Length 709;
Best Local Similarity 28.7%; Pred. No. 1.6e-21;

Matches 100; Conservative 67; Mismatches 141; Indels 41; Gaps 5;
 Qy 144 LLDALADDVVDURGERAAAVDELVARFLPLMKLTFDQQIAMDYVIDSYAQRHLDEIDS 203
 Db 388 LLDIEAD--LADGDRLSYATVSE-----DETGAIKDSINPAIDQ 424
 Qy 204 RQELANAVATHVEAPLSSLEATSQDVAERTTMARDDQVDRMADVSRETSVSASVE 263
 Db 425 LRD-----VSRIHTSQEYARYTQDTOTSNOLAESEHOAQEYAGASTAMNE 473
 Qy 264 VASTADDV-RITSEDABA-----LAQGEAADDALATMIDEATDGVTAGBOLGER 316
 Db 474 MQSIDIQVSANASESAEVAQSVQIASNGAQNQVNSIEGMOTIREQIETSKRIGES 533
 Qy 317 ADVESVTGVDDIATROTNNALNASTEARAGEAEGFAYVADEVKALABESROSTRV 376
 Db 534 SQEIGNIVSLNINDIADOTNIALNAIQASHMAGEAEGFAYVADEVQRLABERSATKQI 593
 RESULT 12
 US-09-252-991A-31412
 ; Sequence 31412, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094, 190
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094, 190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 18744
 ; LENGTH: 573
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-18744
 Query Match 15.6%; Score 373; DB 2; Length 614;
 Best Local Similarity 26.6%; Pred. No. 1. 5e-21;
 Matches 142; Conservative 87; Mismatches 214; Indels 90; Gaps 18;
 Qy 9 VTAADVNRGIDGHALADRG-----LDEABIAWRLSFTG-IDDMMALAAEQPLFEA 59
 Db 108 LFGDVR-----AYRELLGGPVRAQIDEA---NLQFRGQVQEWKVLRLGRO---- 152
 Qy 60 TADALVDFYDILESYR-TDOLFANSIKTQVOLKEQAEVYLGIGRGEY--DTEVAAQ 115
 Db 153 ABA-QTYKWSPEAQSAHQVQDILGRQLGVSAGELKORVER--REBHRGTQYRG 206
 Qy 116 RARIKGKIHDLVGLGPDVYL-----AVTRYTGGLDADLV-----VADR- 156
 Db 207 RQRF-----LEAGADPIAGDQAVTGDRAITAQMQLRDELHQASDHSSISABRT 260
 Qy 157 -----GEEAAAVDE--LVARFL--PMKMLTDDQIQANDTYIDSYQRLHBDIS 203
 Db 261 MLLGSVLIGASLAVALLSLVNLVNRVLPVORLIEHAQSLSHGDFGERETRKBLGK 320
 Qy 204 RQELANAVATHVEAPLSSLEATSQDVAERTT-----MRARTDDQVDRMADVSREBS 256
 Db 321 LALAANTURDFLVIDFDRRSTRDLSASGSINATSLMAAGTREBFSRSTQVATMQE 380
 RESULT 13
 US-09-252-991A-18744
 ; Sequence 18744, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094, 190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 18744
 ; LENGTH: 573
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-18744
 Query Match 15.4%; Score 368.5; DB 2; Length 573;
 Best Local Similarity 25.0%; Pred. No. 3.1e-21;
 Matches 129; Conservative 89; Mismatches 175; Indels 123; Gaps 15;
 Qy 14 RNGIDGHALADRI GL--DEAELAWRLSFTGIDDDTMALAAEQPLFEA 69
 Db 100 RSLLSGHLBSABOIAIGRNRNDHNRNQAL-----DRVROYAAMOP--GAEALAKVAEF- 149
 Qy 70 DHLESVRTQDFLANSKTVEQLKETQAEVILGLGRGEYDTEYAAQRARIGKIHDLGLG 129
 Db 150 -----ERGYALMSATSRVLSLANSPPSAAQLSYGSDSRQFGMAREVINQD----- 196
 Qy 130 PDVYLGATRYTYGGLDADLVVDRGERAAAVDELVARFL-----PMLKLTFFDQ 183
 Db 197 -----DEMERAAAMADGEASSALGERHRMQLVALVAFGL 231
 Qy 184 IAMDY-----IDSVAQRHID-----EIDSROE-----LAVANAVTH 215
 Db 232 VCLSLVLFPLVTRPLQLRQLRBLIANGDGLVRLEVTSDEPGLGSAFNFLDKL 291
 Qy 216 EAPLSSLEATSQDVAERTTMARDDQVDRMAD-----VSREBISSSASAVEBAST 267
 Db 292 QPLIREVGRVGEVADSGSLAGMTAAN DRLINSEHASYDQVSTAATQMSAHEVARN 350
 Qy 268 ADDVRTESEDEAALQGEAADDALATMIDEATDGVTAGBOLGERAADVSREBIS 327
 Db 351 AQSAQADDARQRQREGANVNEATIEVROLAQEVESSESISQQLQSTASIDVLTVI 410
 Qy 328 DDIACQTNMALNASEAARAGEAEGFAYVADEVKALABESROSTRVVEELVQMOET 387
 Db 411 KGIAEOTNLNLLNAAIEAARAGEOEGFAYVADEVRALARTDOSTKDIQARIERLQAGV 470
 Qy 388 EETVDQDLEVNQVNRIGEGFAYVEAMETLQDITDAEDASGMQEVSTATQEANVTEVA 447

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Run on:	November 23, 2005, 04:50:03 ; Search time 159.851 Seconds					
OM protein - protein search, using sw model						
Title:	US-09-455-978B-2					
Perfect score:	2394					
Sequence:	1 MSNDNTLVTDVNRGIDGH. ATDQQVVRTVEEVRETGVSL 489					
Scoring table:	BLOSUM62					
Gappen:	10.0 , Gapext 0.5					
Searched:	1867569 seqs, 417829326 residues					
Total number of hits satisfying chosen parameters:	1867569					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Post-processing:	Minimum Match 0%					
Database :	Published Applications AA_Main:*					
Result No.	Score	Query	Length	DB	ID	Description
1	329.5	16.7	535	4	US-10-282-122A-66393	Sequence 66393, A
2	399.5	16.7	531	4	US-10-282-122A-66393	Sequence 531, APP
3	386.5	16.1	682	4	US-10-282-122A-66174	Sequence 66174, A
4	374.5	15.6	680	4	US-10-282-122A-66970	Sequence 66970, A
5	371.5	15.5	686	4	US-10-282-122A-68162	Sequence 68162, A
6	361	15.1	644	4	US-10-282-122A-77591	Sequence 77591, A
7	359.5	15.0	891	3	US-09-222-809-5	Sequence 5, Appli
8	356.5	14.9	539	4	US-10-282-122A-51025	Sequence 51025, A
9	348.5	14.6	679	4	US-10-389-647-372	Sequence 372, APP
10	348	14.5	626	4	US-10-282-122A-77066	Sequence 77066, A
11	338	14.1	686	4	US-10-282-122A-52305	Sequence 52305, A
12	332	13.9	547	4	US-10-332-288-28	Sequence 28, Appli
13	326	13.6	641	4	US-10-282-122A-77278	Sequence 77278, A
14	315	13.2	643	4	US-10-282-122A-77602	Sequence 77602, A
15	314.5	13.1	1301	4	US-10-282-122A-69564	Sequence 69564, A
16	313.5	13.1	541	4	US-10-282-122A-77047	Sequence 77047, A
17	308	12.9	845	4	US-10-282-122A-76517	Sequence 76517, A
18	297.5	12.4	1137	5	US-10-450-563-54582	Sequence 54582, A
19	292.5	12.2	531	2	US-08-976-0636-34	Sequence 34, Appli
20	292.5	12.2	531	3	US-09-986D-34	Sequence 986D-34
21	292	12.2	564	4	US-10-330-977-6156	Sequence 6156, APP
22	289	12.1	564	4	US-10-335-977-6157	Sequence 6157, APP
23	289	12.1	655	3	US-09-922-227-462	Sequence 462, APP
24	284	11.9	630	3	US-08-882-227-460	Sequence 460, APP
25	280	11.7	675	4	US-0-335-977-4944	Sequence 4944, APP
26	276	11.5	493	4	US-10-335-977-4944	Sequence 4942, APP
27	273.5	11.4	664	4	US-10-335-977-4943	Sequence 4943, APP
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
RESULT 1						
US-10-282-122A-66393						
Sequence 66393, Application US/10282122A						
GENERAL INFORMATION:						
Publication No. US20040029129A1						
APPLICANT: Wang, Liangbu						
APPLICANT: Zamudio, Carlos						
APPLICANT: Malone, Cheryl						
APPLICANT: Habelbeck, Robert						
APPLICANT: Ohlson, Karin						
APPLICANT: Zvorkind, Judith						
APPLICANT: Wall, Daniel						
APPLICANT: Trawick, John						
APPLICANT: Carr, Grant						
APPLICANT: Yamamoto, Robert						
APPLICANT: Rorsyth, R.						
APPLICANT: Xu, H.						
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms						
CURRENT APPLICATION NUMBER: US/10/282-122A						
CURRENT FILING DATE: 2003-02-20						
CURRENT FILING DATE: 2000-03-21						
PRIOR APPLICATION NUMBER: 60/191, 078						
PRIOR FILING DATE: 2000-03-21						
PRIOR APPLICATION NUMBER: 60/206, 848						
PRIOR FILING DATE: 2000-05-23						
PRIOR APPLICATION NUMBER: 60/207, 727						
PRIOR FILING DATE: 2000-05-26						
PRIOR APPLICATION NUMBER: 60/230, 335						
PRIOR FILING DATE: 2000-09-06						
PRIOR APPLICATION NUMBER: 60/230, 347						
PRIOR FILING DATE: 2000-09-09						
PRIOR APPLICATION NUMBER: 60/242, 578						
PRIOR FILING DATE: 2000-10-23						
PRIOR APPLICATION NUMBER: 60/253, 625						
PRIOR FILING DATE: 2000-11-27						
PRIOR APPLICATION NUMBER: 60/257, 931						
PRIOR FILING DATE: 2000-12-22						
PRIOR APPLICATION NUMBER: 60/267, 636						
PRIOR FILING DATE: 2001-02-09						
PRIOR APPLICATION NUMBER: 60/269, 308						
PRIOR FILING DATE: 2001-02-16						
Remaining Prior Application data removed - See File Wrapper or PALM.						
NUMBER OF SEQ ID NOs: 78614						
SOFTWARE: PatentIn Version 3.1						
SRO ID NO: 66393						
LENGTH: 535						
TYPE: PRT						
ORGANISM: Pseudomonas aeruginosa						
US-10-282-122A-66393						
ALIGNMENTS						
SEQUENCE 246, APP						
SEQUENCE 245, APP						
SEQUENCE 50, APP						
SEQUENCE 49, APP						
SEQUENCE 451, APP						
SEQUENCE 228, APP						
SEQUENCE 6, APP						
SEQUENCE 8500, APP						
SEQUENCE 8501, APP						
SEQUENCE 55498, APP						
SEQUENCE 18563, APP						
SEQUENCE 48577, APP						
SEQUENCE 76556, APP						
SEQUENCE 6249, APP						
SEQUENCE 120, APP						
SEQUENCE 1120, APP						
SEQUENCE 114, APP						

; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 66174
 ; LENGTH: 682
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas aeruginosa*
 ; US-10-282-122A-66174

Query Match 16.1%; Score 386.5; DB 4; Length 682;
 Best Local Similarity 27.5%; Pred. No. 1.2e-14; Mismatches 140; Indels 33; Gaps 4;
 Matches 95; Conservatism 77; ;
 Qy 144 LJDALADDDVVADRGEEAAAVADLFLMLKULTFDQOQIANDTYIDSYQRLHEDIDS 203
 Db 356 LDEIDAD-LADGDLTVAVTVE-----DFTQALANSINTSDQ 392

Qy 204 RQELA--NAVATHVPEAPLSSLSEATSQDAERTDTMARTDDQVDRMADVSSRBISSVAS 260
 Db 393 LRLVELVETINQTAQVQVAAAQETQSTAMHLAE-----ASEHOAQETAGASAINEMAVS 445

Qy 261 VEEVAASTADDVRRTSEDAEALAQGEAADDALATMIDIDEATDGVTVAGVEQLGERADV 320

Db 446 IGDQSANASESSAVAIAKNGNEVWHTNTGMDNIREQIQTDSKRKILGQSSQE 505

Qy 321 ESYVGVDDIAEONMLANALANASTEARAGEASGGFAVVADEVKALABESREOSTRVE 380

Db 506 GDIVSLNLDIADQNTNLALNAIQASMGADAGRGFAVVADEEVORLAERSSAATKQIEALV 565

Qy 381 EQMQAETEETDOLDEBNQRIGGVERVEEAMETLOETDAVEDAASGMQEVSTATDBQA 440

Db 566 KTIQTDTNBAVTSMETTSEVVRGARLAQDAGVALEEEIKVSKWHLAULIQNISNAARQQA 625

Qy 441 VSTEEVAEMVGDDRAGEIAALDDIADATDQVORTVEVRTV 485

Db 626 SSAGHISNMVNQETQSQTSGTATARSIGNLAKMASEMRNSV 670

RESULT 4

US-10-282-122A-69670

; Sequence 69670, Application US/10282122A
 ; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Olsen, Kari
 ; APPLICANT: Zvorkind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forbyth, R.
 ; APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA_034A
 CURRENT APPLICATION NUMBER: US/10/282-122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-05
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625

Query Match 15.6%; Score 374.5; DB 4; Length 680;
 Best Local Similarity 24.2%; Pred. No. 6.1e-14; Mismatches 103; Indels 71; Gaps 12;
 Matches 120; Conservatism 201; ;
 Qy 23 ADRIGLDEAIA-----WRLSTGIDD-DTMALAAQOPFB--ATADALVTFD 68

Db 207 ADPGRGRASQFRGVNLNGMLEGATRTRITQVEDRDAARLAETAELEFFVQSSVDEILETS 266

Qy 128 LQDPIVYGAIVTYTGTGDLADDDVVADRGEEAAAVDELVARFLPLMLKLFDOQIA-- 185

Db 316 L-----LALMSITLIGV-----MVERTNRLORETAQSKERNQTAIMRLDEIENLADG 364

Qy 186 -----MDTVIDSYQRLHEDIDSQVQELA--NAVATHVPEAPLSSLSEATSQDAERTD 234

Db 345 DLTVTASVTEETDGTGAIIDSINTSDQRELVTINLAQEQAVASVETQATMQLS--- 420

Db 421 --AASHQALQISAASATVNDMASLDQVSNASESSAVAERSVAIAKNGNEVWOTIH 477

Qy 295 TMDIDDEATDGVTVAGVEQLGERAADVSVTGVGDDIBOTNMALNALSIEARAGEGEG 354

Db 478 GMNDNIREQIQTDSKRKILGQSSQEIDVSLDDIADQNTNLALNAIQASMGADAGRG 537

Qy 355 PAWADEVKALABESREOSTRVEELVEMQMAETEETDOLDEBNQRIGGVERVEEAMET 414

Db 538 FAVTVADEEVORLAERSSAATKQIEALVIAQNTNEAVTSMETTSEVVRGARLAQDAGVA 597

Qy 415 LQSTIDAVEDAASGMQEVSTATDBQA VSTEEVAEMVGDDRAGEIAALDDIADATDQ 474

Db 598 LGBIEGVSRLBLIESITDAAHQQAB-----AGQISQTMVIIQQTTSQ 643

Qy 475 VRTVEEVETVKGK 489

Db 644 TSGTSATASBESIGNIA 658

RESULT 5

US-10-282-122A-68162

; Sequence 68162, Application US/10282122A
 ; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Olsen, Kari
 ; APPLICANT: Zvorkind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forbyth, R.

RESULT 7
 US-09-272-809-5
 ; Sequence 5, Application US/09272809
 ; Patent No. US2002002239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labarias, John C.
 ; TITLE OF INVENTION: Phytofluors as fluorescent labels
 ; FILE REFERENCE: 2500_118US0
 ; CURRENT APPLICATION NUMBER: US/09/272,809
 ; CURRENT FILING DATE: 1998-03-19
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 891
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: cphs locus SLL0041
 ; OTHER INFORMATION: (locus 1001300) an 891 aa protein
 ; OTHER INFORMATION: methyl-accepting chemotaxis protein I. Homology
 ; OTHER INFORMATION: to tsr in last 250 aa.
 ; US-09-272-809-5

Query Match 15.0%; Score 359.5; DB 3; Length 891;
 Best Local Similarity 27.1%; Pred. No. 6.3e-13; Matches 136; Conservative 86; Mismatches 197; Indels 83; Gaps 19;

Db 415 YSBIASNATAETANQASGNADQGRNVNKAKETATRSLADHENTGKVLELASTQEI 474
 Qy 475 GSILDARGISQISQTLNMLALNAAEAAQAGD-DQGRFATVNLASRTAATETQMI 534
 Db 381 EONQAEETETVQDLEVNQRCGGVERVEAMETLOETDAVEDAAGMQE-STATDEQA 440
 Qy 355 FNGPIEKTHQSTKDOVAQTSRERLOVAARGCVSRLVHDNSQORDQIQVTAINGAT 414
 Db 261 VEVVASTADDVRTSBEAALQAGQBAADDALATMDIDBATDGVTAGVQGLGERADV 320
 Qy 441 VSPEEVAAEMVGDVDRAGEIAALDDTADATDQQVRTVEEVETVGKL 488
 Db 595 TVVHTINQNEEINAINEVTTSTAELADAS-----KSLRLBSGRL 635

RESULT 8
 US-10-282-122A-51025
 ; Sequence 51025, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Lianguo
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forbyth, R.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELUTRA-034A
 ; CURRENT APPLICATION NUMBER: US/10/282.122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 51025
 ; LENGTH: 539
 ; TYPE: PRT
 ; ORGANISM: Bordetella pertussis
 ; US-10-282-122A-51025

Query Match 14.9%; Score 356.5; DB 4; Length 539;
 Best Local Similarity 26.6%; Pred. No. 5.3e-13; Matches 234; Conservative 81; Mismatches 153; Indels 113; Gaps 15;

Db 627 DNEVAVROLAQANRQALVAEALRQMKNSIOAVENAAQASAVQRAOTVDOE 686
 Qy 571 L-LMEVDPVSRGLDTIRAVV-TDEDEGTIADSNTATSLRRTVQVTAQSFTET 626
 Db 287 AAADDALATMDIBATDGVTAGVQGLGERADVDESVTGVTAGDQIAEQTMALNAAESTEA 346
 Qy 687 DAMNRTVGDIVAIRETVAATAKOVERGEGSOKSKVUNLIGSPADQTMALNAAESTEA 746
 Db 347 RAGEAGEGFAVVAEVLAKLAEBSREQSTREVELVQMQBETTEETVQDQDDEVNQRIGEV 406

Db 747 HAGEEGRFQAVVADAEVSLAROSAETATETAQALVATIQAETNEVNVNAAEGTEQQVVGTK 806
 Qy 407 RVEEAMETLQETDADAEASGMQE VSTATDQAVSTEE-----VAEMD----- 451
 Db 807 LVEETRRLSNQQT-AVSAQISQGLVETATSALEQQTSESVTQTMALVQJADKNSSEAS 865
 Qy 452 GVDRAEGRIAALDDTADATDQ 473
 Db 866 GVSATFELLAVAQSQILOBAVKQ 887

Query Match 14 1%; Score 338; DB 4; Length 686;

US-10-282-122A-52305

RESULT 11

; Sequence 52305, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Habelbeck, Robert

APPLICANT: Olsen, Kari

APPLICANT: Zverkkind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELTRA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PAMM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 52305

LENGTH: 686

TYPE: PRT

ORGANISM: Clostridium botulinum

US-10-282-122A-52305

RESULT 12

; Sequence 28, Application US/10332288

Publication No. US20040051165A1

GENERAL INFORMATION:

APPLICANT: RAYNER, Paul Barton

APPLICANT: SPIERS, Andrew Julian

APPLICANT: BANTINAKI, Eleni

TITLE OF INVENTION: BACTERIAL POLYSACCHARIDE AND BIOFILM DEVELOPMENT

FILE REFERENCE: 10317-70012US00

CURRENT APPLICATION NUMBER: US/10/1332,288

CURRENT FILING DATE: 2003-10-06

PRIOR APPLICATION NUMBER: PCT/GB01/03077

PRIOR FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: UK 0016842.7

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 28

LENGTH: 547

TYPE: PRT

ORGANISM: Pseudomonas fluorescens

US-10-332-288-28

Query Match 13.9%; Score 332; DB 4; Length 547;

Best Local Similarity 25.0%; Fred. No. 1.5e-11; Mismatches 189; Indels 84; Gaps 12; Matches 119; Conservative 84; Mismatches 189; Indels 84; Gaps 12;

QY 66 TDFYHLESVERTQDLPANSTKTVBQLKTCQAELYLGLGRGEYDTEYAA----- 114

QY 89 TDKDNYKSPEARIEQMANVYKTI---HGQD-----RMPDNPKAAHINYNKVLAQV 138

QY 115 -QRAIGKTHDVLGLGPDVYIAGYRTYVYTGILDALADDV-VADRGEEAAADVELV--- 168

QY 139 IERVEANDLPGANOLBLEQITPIWTEGRMKNLNDITENKNSDR---ATAHDEAIVSAK 195

Db 169 ------ARFLPMKLLTFDQIQMDTYD-SYARLH---DE 200

Db 196 ISMAYSLILAILAAGLGLLIMRAIMAPMORIVDI----LETMRDGDLSKRLNLERKDE 250

QY 201 1DSRQELANAVATHYAPLSSLEATSQDAARTDMTRARTDDQVDRMDSREISSVAS 260

Db 251 FGAVERGFGNDMMTTELAVSQAORSSVQVTTSVTIAATSKQQTATATAATTBEGAT 310

QY 261 VEEVASTADDVRTSBDAAALAQGEEAA---DDALA---TMDIDEATDGVIGVEQL 313

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Db 256 KQLTIRNE-----MDLVKD----SEVLLKADEMSAAVIALKGSESVQAA 300
Qy 314 GERAADVESVTGVIDDIAEQTNMLANASTEARAGEAGEGPAVVADEVKALBESREQS 373
Db 371 NEKAGNINQVVTIVKVDQNLNSINAEEAKAGEYGGFAVIAVERLLAQATAV 430
Qy 374 TRVEELVEQMAETEETDODIDEVNORIGBEGVERVEAMTLOEITDAVEDAASGMQEV 433
Db 431 YDIEQMREIQSAVSAVGVMGMDFKSFSEVRROMFVQVNGEOLSQITHQVQALAPRVLVN 490
Qy 434 TATDEQAVSTEVAAEMVGUDRAGIAAADDIADATDQVRTVEEVTGKLS 489
Db 491 EGMQADATGAPQINH-----ALVQGDASSOTVESLROASFAIDEL 532
Qy 572 SKRISBESAGGIERSTADARAGMDDIATAEESHTGEEATAAROQSSTSSELASAINI 631
Db 632 AAVADE 637

Db 393 GITSITQEQGARIGKERAESLICAKENMLTGEBENKTTUDMILATFESTKATENLINE 452
Qy 316 RAADVESVTGVIDDIAE-----QTNMLANASIEAARAGEAGEGPAVVADEVKALB 368
Db 453 -MANIERISRQIDKIVDGISINVSIQTMALAVNGAVEAARAGEYKGFAVUSTDIONLAND 511
Qy 369 SREQSTRVBLVEQMAE-----TE-----TVDQDLEBNQHIGEYER 407
Db 512 AAENAEQOKDQVNTOEQNINVRKDLADILSTWEEQAKALTIKQLDNVRSRMSDVILG 571
Qy 408 VEEAMTLOEITDAVEDAASGMQVSTATDEQAVSTEVAAEMVGUDRAGIAAADDI 467
Db 572 SKRISBESAGGIERSTADARAGMDDIATAEESHTGEEATAAROQSSTSSELASAINI 631
Qy 468 ADATDQ 473
Db 632 AAVADE 637

RESULT 13
US-10-282-122A-77278
; Sequence 77278, Application US/10282122A
; Publication No. US2004029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Hasebeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forstb, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 77278
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; US-10-282-122A-77278

Query Match 13.6%; Score 326; DB 4; Length 641;
Best Local Similarity 24.1%; Prd. No. 4e-11;
Matches 117; Conservative 97; Mismatches 164; Indels 108; Gaps 16;
Qy 45 DTWALALAACQPLFEATADALVTFDHLFESYERTDQFLANSTKTCVEQLKETOE---- 98
Db 203 DTVRLAEEKAEEKANNTESLILQDNGAE-----MWSNGVKSQRAESEVQKGVN 255
Qy 99 YLGGLGRGIDYTAQARAKRIGKHDVIGLSPDVLGATRTVYTGJAL-----ADDVADRG 157
; Remaining Prior Application data removed - See File Wrapper or PALM.

```

NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2762
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; US-10-282-122A-77602
; Query Match 13.2%; Score 315; DB 4; Length 643;
; Best Local Similarity 24.9%; Pred. No. 1.8e-10;
; Matches 100; Conservative 77; Mismatches 167; Indels 58; Gaps 10;
; Qy 133 YLG-AYTRYVYGLDALLADD-----VVADRGSEAAAVDELVAR----- 170
; Db 249 YLGIEFDQYKRV-NLFDMMWMLMVFVDKA-TALAVDYAVANAITGIVLIGISVG 305
; Qy 171 -----FLPMLKLTFDQOIQIAMDYIDSYAOQLHDEIDSROBLAN----- 209
; Db 306 IIFTINQTYKPLURLKVAVIDLAGGS-GDLTRLL-BINGNDLALQISEGFNRPSGILQ 361
; Qy 210 ---AVATHVEAPLSSLEATSQDVIAERTDTMRDQVDRMADVSEISSVSVASVERVA 265
; Db 362 NMMLQISIATQIISSSIEGLSQ-TAKENQMLISHSETDQ--VVTATOMSARTVA 417
; Qy 266 STADDVRRTSEDAEALAOQGEAAADDALATMWDIDDEATDGTAGVQGEVQGERAADVSVTG 325
; Db 418 ESYTQSQNITEAASKEAQOSLIVINNAIVTSLVNDVENMSEISNMNRDANKISEVL 477
; Qy 326 VDIDIAEOTNMALANASIAARAGEAGEGFAVVADEKVALAEEBSRQSTRVEELVQMOA 385
; Db 478 VIGALSEQNTMLANAAEARAGEQGRFAVVADEBVALAARTQNSTEISDMLTKL 537
; Qy 386 ETEFTVDQDLEBNVNRIGEYVERVEAMETLQITDAVEDAASGMQEVSSTATDEQAVSTEE 445
; Db 538 GTDSWVGAMERTKQSCQTTADKTSBVSQSGSLNMMSASVSDIDLTQIAATEQOSTVAE 597
; Qy 446 VAENWDGVIDRAGEIAAALDDIADTDQQVRTVEFREVVGK 487
; Db 598 LSRNMWLSIREIVESIIVNSGRQTVGATESLSHSNHELEQLVKG 639
; RESULT 15
; US-10-282-122A-69564
; Sequence 69564 Application US 10282122A
; Publication No. US20040023129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangs
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haezelbeck, Robert
; APPLICANT: Ohlson, Kari
; APPLICANT: Zverkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA_034A
; CURRENT APPLICATION NUMBER: US 10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,079
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-05-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/242,578
; SEQ ID NO: 69564
; LENGTH: 501
; ORGANISM: Pseudomonas syringae
; US-10-282-122A-69564
; Query Match 13.1%; Score 314.5.; DB 4; Length 501;
; Best Local Similarity 27.4%; Pred. No. 1.4e-10;
; Matches 86; Conservative 59; Mismatches 136; Indels 33; Gaps 5;
; Qy 176 KLLTFDQIAMDYID-----SYAQQLHDEIDSROBLANAVTHVEAPLSSLEATSQD 228
; Db 184 RMLATTNQSPPSDKIDERSGKHKSLAQRFQFLAQITGIVDGVWRDTR---GIGELGHD 239
; Qy 229 VAERTDTMR-----ARTDDQDVRMADVSRBIISS-VSASVEBAAVSTADDYRTSED 277
; Db 240 LAKASGTLETGQHQHOLSETARMTGAMQRMGAMDISGHVAQAVQRAGDASDQV----- 293
; Qy 278 AEAALAQQGEAAADDALATMWDIDDEATDGTAGVQGEVQGERAADVSVTG 337
; Db 294 ---AHGRDUSVDRQSEBTQOALARISTTDTQVLANOSEQIGKLVDSIABOTNL 348
; Qy 338 ALNAAIEAARAGEAGEGFAVVADEKVALAEEBSRQSTRVEELVQMOA 397
; Db 349 ALNAAIEAARAGEQGRFAVVADEBVALAARTQNSTEISDMLTKL 408
; Qy 398 NORIGEYVERVEAMETLQITDAVEDAASGMQEVSSTATDEQAVSTEEVAVMDGVDDRA 457
; Db 409 1QGVGRCVENSQRASESLSRSVEGEGIGHITOLNLGIATTEQQATASREIADQLRSVQIA 468
; Qy 458 GEIAALDDIADAT 471
; Db 469 EHTAAANIGVLAASS 482
; Search completed: November 23, 2005, 05:09:01.
; Job time : 161.851 SECs

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